



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95712

TO: Shin-Lin Chen
Location: cm1/12a15/12e12
Art Unit: 1632

June 6 2003

Case Serial Number: 788188

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:52 ; Search time 15 Seconds

(without alignments)
1544.560 Million cell updates/sec

Title: US-09-788-188-2

Sequence: 1 MSMLFYTLITAFILGIGQAP.....FIRIDPACVCVSRKAVRRA 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1265	99.8	286	1	NGHUBM
2	1119	88.2	229	2	nerve growth facto
3	1102	86.9	245	2	nerve growth facto
4	1091	86.0	307	1	nerve growth facto
5	1087	85.7	241	2	nerve growth facto
6	1068	84.2	303	1	nerve growth facto
7	783.5	61.8	243	2	nerve growth facto
8	768	60.6	235	2	nerve growth facto
9	671.5	53.0	243	2	nerve growth facto
10	658	51.9	125	2	nerve growth facto
11	644	50.8	246	2	nerve growth facto
12	484	38.2	117	2	nerve growth facto
13	481.5	38.0	194	2	nerve growth facto
14	476.5	37.6	257	2	nerve growth facto
15	467	36.8	258	2	nerve growth facto
16	466.5	36.8	257	2	nerve growth facto
17	466	36.8	282	2	nerve growth facto
18	452.5	35.7	116	1	nerve growth facto
19	448.5	35.4	116	2	nerve growth facto
20	426	33.6	286	2	nerve growth facto
21	365	28.8	247	2	nerve growth facto
22	364	28.7	249	2	nerve growth facto
23	360	28.4	249	2	nerve growth facto
24	358.5	27.5	252	2	nerve growth facto
25	348.5	26.7	248	2	nerve growth facto
26	338	26.4	236	2	nerve growth facto
27	335	26.4	269	2	nerve growth facto
28	332.5	26.2	210	2	nerve growth facto
29	325.5	25.7	209	2	nerve growth facto

30	323.5	25.5	114	2	184765	brain-derived neur
31	316.5	25.0	114	2	150606	brain-derived neur
32	307.5	24.3	114	2	151599	brain-derived neur
33	86	6.8	397	2	852783	aspartic proteinas
34	83.5	6.6	5126	2	840450	ryanodine receptor
35	82.5	6.5	749	2	886774	hypothetical prote
36	81.5	6.4	701	2	152384	hypothetical prote
37	81.5	6.4	1076	2	D82083	cardamoyl-phosphat
38	80	6.3	2535	2	AC0304	probable hemolysin
39	79.5	6.3	481	2	T27665	hypothetical prote
40	79.5	6.3	1609	2	E87243	probable induced tr
41	79	6.2	807	2	A53225	ecdysone-induced p
42	79	6.2	835	2	C97322	probable alpha-ara
43	78.5	6.2	357	2	T06622	hypothetical prote
44	78.5	6.2	480	1	TWMTGC	phosphoglycerate k
45	78	6.2	323	2	869647	hypothetical prote

ALIGNMENTS

RESULT 1

NGHUBM

nerve growth factor beta chain precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999

C/Accession: A01399; S10253

R/Unlrich, A.; Gray, A.; Berman, C.; Dull, T.J.

Nature 303, 821-825, 1983

A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mouse

A/Reference number: A93305; MUID:83244969; PMID:6688123

A/Accession: A01399

A/Molecule type: DNA

A/Residues: 1-286 <URL>

R/Borant, G.; Pizutti, A.; Rugerli, E.I.; Falini, A.; Silani, V.; Sidoli, A.; Scarlato

Nucleic Acids Res. 18, 4020, 1990

A/Title: cDNA sequence of human beta-NGF.

A/Reference number: S10253; MUID:90326556; PMID:2374737

A/Accession: S10253

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 46-286 <BOR>

A/Cross-references: EMBL:X52599; NID:G29476; PIDN:CA36832.1; PID:G29477

C/Comment: Nerve growth factor is found in submaxillary gland in large quantities and i

nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels ma

C/Genetics:

A/Gene: GDB:NGFB

A/Cross-references: GDB:120233; OMIM:162030

A/Map position: 1p13.1-1p13.1

A/Introns: 41/3

C/Complex: nerve growth factor is composed of two alpha chains, two beta chains, and tw

C/Superfamily: nerve growth factor beta chain

C/Keywords: glycoprotein; growth factor; submandibular gland

F.1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>

F.167-284/Product: nerve growth factor beta chain #status predicted <MAT>

F.126-114,159,211/Binding site: carbohydrate (Asn) (covalent) #status predicted

F.181-246,224-274,234-276/Disulfide Bonds: #status predicted

Db	106	ARVAGQNTNITVDPRLEFCGRRLRSPVLFSTQPPREADITQDDLEFGGAAPFNRTRSK	165
Qy	121	RSSHPIDHGEFSVCDSSVVMGDKTTATDIIKGEVMVLGEVINNSVFKQYFFETKCR	180
	166	RSSHPIDHGEFSVCDSSVVMGDKTTATDIIKGEVMVLGEVINNSVFKQYFFETKCR	225

Qy	1	MSMLFYTLITAFILGIGQAPHSSENVPAAGHTIPQVHTKLOHSIDTLRPARSAPAAIA	60
Db	46	MSMLFYTLITAFILGIGQAPHSSENVPAAGHTIPQVHTKLOHSIDTLRPARSAPAAIA	105
Qy	61	ARVAGQFRNTIVDPRLFKKRLRSPTLPSTOPREAADQODLDFEYGAAPSRTRSK	120
Db	106	ARVAGQFRNTIVDPRLFKKRLRSPTLPSTOPREAADQODLDFEYGAAPSRTRSK	165
Qy	121	RSSSHPIFHRGEFSVCDVSVMWGDKTTATDINGKEVMVLGEVNNINSVFKQYFFETKCR	180
Db	166	RSSSHPIFHRGEFSVCDVSVMWGDKTTATDINGKEVMVLGEVNNINSVFKQYFFETKCR	225

A/Accession: S12532
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 126-243 <IBA>
C/Superfamily: nerve growth factor beta chain
C/Keywords: growth factor
F/1-125/Domains: signal sequence #status predicted <Sig>
F/126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match	61.8%;	Score 783.5;	DB 2,	Length 243;
Best Local Similarity	64.5%;	Pred. No. 4.9e-66;		
Matches 160;	Conservative 21;	Mismatches 48;	Indels 19;	Gaps 6;

Qy	1	MSMLFYLLIAFLAFIGIOAEPSHSSN----	VPAGHTIPQVHWKLOHSLDTALBPBARAPA	56
Db	5	MSMLYLLIAFLAFIGIOAAPSSEDNPLEPRL	ELHSLPSTQSGNGHT-----AKAAPQ	57
Qy	57	AALAAARA-----GQIRNITVDPRLEFKKRL	RLSPVLPSTOPPREADTODLDFEVGAA	111
Db	58	TT-HGRAAMPDGTBTLNIA MQNPFKKRR	PFSSHYLSTPTOPPPVRKQSGTGF-LSAAV	115
Qy	112	PSRTRHSKSSKSHPIFRHGGEPSCVSVWV	GDGKTATDILKGKXWMLGAVNNVNSVFK	171
Db	116	SLNRITARTGR-TNHPVLRHGEZPSVCD	SVSMVGDGKTATDILKGKXVYLVGAVNNNVFK	174
Qy	172	QYEPFETKCDPNPNVDSGCGRIDSKHNSY	CYTHHTFVYALITMDGKQAAAREIRIDTACVC	231
Db	175	QYEPFETKCDPNPNVDSGCGRIDAKHNSY	CYTHHTFVYALITMDGKQAAAREIRIDTACVC	234
Qy	232	VLRSKXAVR	239	
Db	235	VLRSKSGR	242	

RESULT 8
S14481

C/Species: *Xenopus laevis* (African clawed frog)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
 C/Accession: S14481
 C/Contributor: F. Campion, M. Cardinal, B. Pierandrei-Amaldi, P. submitted to the EMBL Data Library, October 1990
 A/Description: Structure and expression of the nerve growth gene in *Xenopus* oocyte and
 A/Reference number: S14481
 A/Accession: S14481
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-235 <CAR>
 A/Cross-references: EMBL:X55715, NID:g64914, PIRN:CAA39249.1, PID:g64915
 C/Superfamily: nerve growth factor beta chain

Query Match	60.6%;	Score 768;	DB 2;	Length 235;
Best Local Similarity	63.2%;	Pred. NO. 1.3e-64;		
Matches 153; Conservative	28;	Mismatches 41;	Indels 20;	Gaps 6

[illegible]

Db 231 RK 232

RESULT 9
T51193

nerve growth factor precursor - many-banded krait
 C/Species: Bungarus multicinctus (many-banded krait)
 C/Date: 13-Sep-1996 #sequence_rev15193
 C/Accession: 151193
 R/Danse, J.M.; Garnier, J.M.
 Growth Factors 8, 77-86, 1993
 A/Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the
 A/Reference number: 151193; MOID:93192074; PMID:7916740
 A/Accession: 151193
 A/Status: preliminary; translated from GB/EMBL/DBST
 A/Molecule type: mRNA
 A/Residues: 1-243 <DAN>
 A/Cross-references: GB:I566212; NID:g266298; PIDN:AAB25729.1; PID:g266299
 C/Superfamily: nerve growth factor beta chain

Query Match	53.0%	Score 671.5;	DB 2;	Length 243;
Best Local Similarity	56.1%	Pred. No. 1.6e-55;		
Matches 138;	Conservative 29;	Mismatches 62;	Indels 17;	Gaps 5

Qy	1	MSMFLYLITAFILGIOAEPSSESNVPAG----	HTIPGVHTKLGHSIDTALRRASABA	56
Db	1	MSMLCYLILAFILGIMAAPKSEDNVPLGSAKXDFSTNCQAHTEGLKTSKNTDHHPT		60
Qy	57	AAIAA-RVAGQTRNITVDPRLEFKTRRLSPVLVSTOOPREAAQTOD---	LDPEVGAAP	112
Db	61	PKKSEDELCSAANIIVDPKLFQKRRFQSPVLVSTOOPPLSRDEQSVKFLDTE-----		114
Qy	113	FSRTHRS--KRSSHPIFRHGEFECVCSVSYVWDKXTATCTIKGKENVVLGSEVNLNNSVF		170
Db	115	-DLNRRITAMNNENHPVHNGSEHSVCDSISVWVNNKTKATDIKGVTVVWVDVNNINNEY		173
Qy	171	KQYFFETKCDPNPVDGCRGIDSKHNSYCTTHTTEFKALTMDCQAAKRFIRIDTACV		230
Db	174	KQYFFETKCPNPVPFSGCRGIDSRHNSYCTTTDTFKALTMGNRAKSMRIRIDTACV		233
Qy	231	CYLSRK	236	
Db	234	CYLSRK	239	

RESULT 10

nerve growth factor beta chain precursor - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 19-Nov-1988 #sequence_rev1stion 19-Nov-1988 #ext_change 16-Jul-1999
 C/Accession: A26312
 R/Meter: R.; Becker-Ande, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
 EMBL J. 5, 1489-1493, 1986
 A/Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
 A/Reference number: A26312; MUID:86300647; PMID:2427334
 A/Accession: A26312
 A/Molecule type: mRNA
 A/Residues: 1-125 <ME1>
 A/Cross-references: GB:M26609; NID:G163419; PIDN:AAA0666.1; PID:G163420
 C/Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embry
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: growth factor; homodimer; seminal vesicle
 F:6-125/Product: nerve growth factor #status predicted <MAT>
 F:20-85,63-113,73-115/Dissulfide bonds: #status predicted

Query Match	51.9%	Score 658;	DB 2;	Length 125;
Best Local Similarity	95.2%;	Pred. NO. 1.3e-54;		
Matches 119; Conservative	4;	Mismatches 2;	Indels 0;	Gaps 0

Qy 117 HSKRSSHPHFHGEFSYCDSVSMVGDTATDICKKEMVLGSENNINNSVFQKYFFE 176
| | | | : | | | | : | | | | | | | | | | | | | | |
Db 1 HSKRSSHPFVFRHGEFSYCDSIWMVGDKTTATDIKGKVMVLGSENNINNSVFQKYFFE 60

Qy 177 TKCDPVPVDSGCGIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 236
 Db 61 TKCDPVPVDSGCGIDAKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 120
 Qy 237 AVBRA 241
 Db 121 TQORA 125

RESULT 11

A59218

nerve growth factor beta chain precursor - monocled cobra
 C/Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 C/Accession: A59218; S13965

R/Selby, M.J.; Edwards, R.H.; Rutter, W.J.
 J. Neurosci. Res. 18, 293-298, 1987

A/Title: Cobra nerve growth factor: structure and evolutionary comparison.
 A/Reference number: A59218; MUID:88090976; PMID:3694712

A/Accession: A59218

A/Molecule type: mRNA

A/Residues: 1-246 <SEL>

R/Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.
 FEBS Lett. 279, 38-40, 1991

A/Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
 A/Reference number: S13927; MUID:91138755; PMID:1995338

A/Accession: S13965

A/Molecule type: protein

A/Residues: 131-246 <INO>

A/Experimental source: Venom

C/Comment: Nerve growth factor is necessary for the development of embryonic sympathetic

C/Complex: homodimer

C/Superfamily: nerve growth factor beta chain

C/Keywords: growth factor; homodimer; venom

F/1-23/Domain: signal sequence #status predicted <SIG>
 F/131-246/Product: nerve growth factor beta chain #status experimental <MAT>
 F/144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match 50.8%; Score 644; DB 2; Length 246;
 Best Local Similarity 55.2%; Pred. No. 6, 4e-53;
 Matches 133; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

Qy 1 MSMFLYTLITLALIGIOAPHSSESNYPAG---HTIPQVHWTKQHSIDTLARASAA 56
 Db 6 MSMFLYTLITLALIGIWAPESEDNVPLGSPATSDLSCTQTEHGLTSRNTDHPA 65
 Qy 57 AAIARVAGQT-RNTTVDPRFLFKKRLRSFVLPSTQPREADTQDLPFVGAAPFAR 115
 Db 66 FOKEDQELRTFANIIYDPLFKQKQFQSPFVLPSTQPREADTQDLPFVGAAPFAR 124
 Qy 116 THRSRSSHPIFRHGESVCSVSWVGDKTATADIKKEVWVAGEVINNSVFQYF 175
 Db 125 NTRAR-BDHVPHNIGHSVCSVSAWV-TKTATADIKNTVTVMENVALDNKYKQYF 182
 Qy 176 ETTCRDPVPVDSGCGIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 235
 Db 183 ETTCRDPVPVDSGCGIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 242
 Qy 236 K 236
 Db 243 K 243

RESULT 12

S28161

nerve growth factor beta chain - Russell's viper
 C/Species: Vipera russelli (Russell's viper)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C/Accession: S28161

R/Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.
 Biochim. Biophys. Acta 1160, 287-292, 1992

A/Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A/Reference number: S28161; MUID:93120151; PMID:1477101

A/Accession: S28161
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-117 <KOY>
 C/Superfamily: nerve growth factor beta chain

Query Match 38.2%; Score 484; DB 2; Length 117;
 Best Local Similarity 74.1%; Pred. No. 2, 8e-38;
 Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

Qy 125 HPFRHGEFVCSVSWVGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNP 184
 Db 1 HPFRHGEFVCSVSWVANKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNP 60
 Qy 185 VDSGCGIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 236
 Db 61 VDSGCGIDAKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 112

RESULT 13

I51709

nerve growth factor beta chain precursor - southern platyfish
 C/Species: Xiphophorus maculatus (southern platyfish)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C/Accession: I51709; S26674

R/Goetz, R.; Raulf, F.; Schardt, M.
 J. Neurochem. 59, 432-442, 1992

A/Title: Brain-derived neurotrophic factor is more highly conserved in structure and fi
 A/Reference number: I51708; MUID:92333301; PMID:1629719

A/Accession: I51709

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-194 <GOT>

A/Cross-references: EMBL:X59941; NID:G65277; PID:CA442566.1; PID:G65278

C/Genetics:

A/Gene: NGF

C/Superfamily: nerve growth factor beta chain

C/Keywords: glycoprotein; growth factor

F/1-14/Domain: signal sequence #status predicted <SIG>
 F/15-79/Domain: propeptide #status predicted <PRO>
 F/80-194/Product: nerve growth factor beta chain #status predicted <MAT>
 F/90-155,133-183,143-185/Disulfide bonds: #status predicted
 F/199/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.0%; Score 481.5; DB 2; Length 194;
 Best Local Similarity 59.3%; Pred. No. 8, 9e-38;
 Matches 99; Conservative 14; Mismatches 39; Indels 15; Gaps 3;

Qy 71 TVDPRFLFKKRLRSFVLPSTQPREADTQDLPFVGAAPFSTRSRSSHPFIR 130
 Db 40 TVDPRFLFKKRLRSFVLPSTQPREADTQDLPFVGAAPFSTRSRSSHPFIR 84
 Qy 131 GEFVCSVSWVGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNPVDSGR 190
 Db 85 GEFVCSVSWVGNKTKATDISGEVTVLPYVINNNVKKQYFETKCRDPNPVDSGR 144
 Qy 191 GIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 237
 Db 145 GIDSKMNSYCTTTHFPVKALTMGQKQAAFRIRIDPACVLSRK 191

RESULT 14

C40304

neurotrophin-3 precursor - human
 N/Alternate names: nerve growth factor 2; NGF-2
 C/Species: Homo sapiens (man)
 C/Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C/Accession: A36208; J0141; C40304; S10719; C60536

R/Jones, K.R.; Reichardt, L.F.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A/Title: Molecular cloning of a human gene that is a member of the nerve growth factor

A/Reference number: A36208; MUID:91045937; PMID:2236018

A/Accession: A36208

A/Molecule type: DNA
 A/Residues: 1-257 <CON>
 A/Cross-references: GB:X53763; NID:G189300; PIDN:AAA5993.1; PID:G189301
 R.Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nikolic
 Neuron 4, 767-773, 1990
 A/Title: Primary structure and biological activity of a novel human neurotrophic factor.
 A/Reference number: JH0141; MUID:90262727; PMID:2344409
 A/Accession: JH0141
 A/Molecule type: DNA
 A/Residues: 1-257 <ROS>
 R.Maisompierre, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la M
 Genomics 10, 558-568, 1991
 A/Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struct
 A/Reference number: A40304; MUID:9165361; PMID:1889806
 A/Accession: C40304
 A/Molecule type: DNA
 A/Residues: 1-257 <MAI>
 A/Cross-references: GB:M61180; NID:G189302; PIDN:AAA63231.1; PID:G189303
 R.Kaibho, Y.; Yoshimura, K.; Nakahama, K.
 PNAS Lett. 266, 187-191, 1990
 A/Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.
 A/Reference number: S10719; MUID:90306351; PMID:2365067
 A/Accession: S10719
 A/Molecule type: mRNA
 A/Residues: 1-257 <KAI>
 A/Cross-references: GB:X53655; NID:G287794; PIDN:CAA37703.1; PID:G287795
 R.Yancopoulos, G.D.; Maisompierre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
 A/Title: Neurotrophic factors, their receptors, and the signal transduction pathways the
 A/Reference number: A60536; MUID:9211157; PMID:1966766
 A/Accession: C60536
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-73, 'Q', '75-77', 'R', '79-108', 'T', '110-257' <YAN>
 A/Accession: GDB:NTF3
 A/Genetics:
 A/Cross-references: GDB:125917; OMIM:162660
 A/Map position: 12p13-12p13
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein
 F.1-18/Domain: signal sequence #status predicted <SIG>
 F.19-138/Domain: propeptide #status predicted <PRO>
 F.139-257/Product: neurotrophin-3 #status predicted <MAT>
 F.131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.6%; Score 476.5; DB 2; Length 257;
 Best Local Similarity 40.3%; Pred. No. 3.7e-37;
 Matches 106; Conservative 38; Mismatches 88; Indels 31; Gaps 6;

QY 1 MSMLFYTLITAFILGIGIAEPHSESNVPAHTIPQV-----HWTKLQSLD 45
 Db 1 MSILFYIYFLAYLGIQGNMMDQSLPDSLSLSILIKLQADILKNKLSKOMVDVKNYQ 60
 QY 46 TALRA-----RSAPAAIAARVAGQTRNITVDPRLFK-KRLRSPRYLFSPTOPREA 97
 Db 61 STLPKAPRPEPEQGEATRSEFPQMIATDTLRLQGRVNSPRLVLSOSTLEBPPLYM 114
 QY 98 ADTODLPEVGAAPFRTHSRKSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEY 157
 Db 115 PPLVMDYVGSFVVARTRRKYAEHK-SHRGEISVCSSESLMTDKSSAIDIRGHQV 173
 QY 158 MVLGEVINNSVFQYFETKCRDPNPVDSGCRGIDSKHNSYCTTTHFEVKALTMW-GK 216
 Db 174 TVLGEITGNSPVQYFETKCRKAPVKNCGRGIDDKHNSQCKTSQTVVRLTSENK 233
 QY 217 QAARFIRIDTACVCVLSRKAVR 239
 Db 234 LVGKRWIRIDISCVALSRKIGR 256

RESULT 15
 S09155
 neurotrophin-3 precursor - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
 C/Accession: S09155; S51179
 R.Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.
 Nature 344, 333-341, 1990
 A/Title: Identification and characterization of a novel member of the nerve growth fa
 A/Reference number: S09155; MUID:90190865; PMID:2314473
 A/Accession: S09155
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-258 <HON>
 A/Cross-references: GB:X53257; NID:G53451; PIDN:CAA7348.1; PID:G53452
 R.Kolbeck, R.; Jungbluth, S.; Barde, Y.A.
 Eur. J. Biochem. 225, 995-1003, 1994
 A/Title: Characterization of neurotrophin dimers and monomers.
 A/Reference number: S51179; MUID:95045576; PMID:7957235
 A/Accession: S51179
 A/Status: Preliminary
 A/Molecule type: protein
 A/Residues: 140-152 <KOL>
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein
 F.1-18/Domain: signal sequence #status predicted <SIG>
 F.140-258/Product: neurotrophin-3 #status predicted <MAT>
 F.131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.8%; Score 467; DB 2; Length 258;
 Best Local Similarity 41.5%; Pred. No. 2.9e-36;
 Matches 107; Conservative 34; Mismatches 97; Indels 20; Gaps 5;

QY 1 MSMLFYTLITAFILGIGIAEPHSESNVPAH-----TIPOVHWTKLQSLDITL----- 48
 Db 1 MSILFYIYFLAYLGIQGNMMDQSLPDSLSLSILIKLQADILKNKLSKOMVDVKNYQ 60
 QY 49 -----RRASAPAAIAARVAGQTRNITVDPRLFKKRLRSPRYLFSPTOPREAADTDL 103
 Db 61 STLPKAPRPEPEQGEATRSEFPQMIATDTLRLQGRVNSPRLVLSOSTLEBPPLYM 120
 QY 104 DFEVGAAPRSRTH-REKSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEYVNLGE 162
 Db 121 EDVYGNVAVNRSPRKRKYAEHK-SHRGEISVCDSSSLMTDKSSAIDIRGHQVTVLGE 179
 QY 163 VNINNSVFQYFETKCRDPNPVDSGCRGIDSKHNSYCTTTHFEVKALTMW-GKQAMR 221
 Db 180 IKTGNSPVQYFETKCRKAPVKNCGRGIDDKHNSQCKTSQTVVRLTSENKLVGWR 239
 QY 222 FIRIDTACVCVLSRKAVR 239
 Db 240 WIRIDISCVALSRKIGR 257

Search completed: June 6, 2003, 10:51:33
 Job time: 15 secs

GenCode version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:28 ; Search time 27 Seconds
(without alignments)
1839.161 Million cell updates/sec

Title: US-09-788-188-1
Perfect score: 1270
Sequence: 1 MSMLFYTITATLFIQIQAEP.....FIRIDRACYCULSRKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioid:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	99.7	241	4	Q9UKL8
2	1265	99.6	241	4	Q9P2Q8
3	1258	99.1	241	4	Q96P60
4	1249	98.3	241	6	Q9N2P0
5	1247	98.2	241	6	Q9N2P1
6	1247	98.2	241	6	Q9N2P2
7	1132	89.1	217	6	Q9N1B3
8	1038	81.7	294	11	Q91XB4
9	713	56.1	241	13	Q9D8Z9
10	709	55.8	241	13	Q9D8Z8
11	462	36.4	87	4	Q9PTC3
12	459	36.1	87	4	Q9P2Z4
13	449.5	35.4	132	11	Q9W015
14	426.5	33.6	241	6	Q9N1B2
15	426	33.5	286	13	Q91988
16	363	28.6	247	6	Q97759

17	360	28.3	249	11	Q8VHH4	Q8VHH4 mus musculus
18	342.5	27.0	246	13	Q8G374	Q8G374 cyclophilops
19	341.5	26.9	246	13	Q8G376	Q8G376 jalapura sp
20	339.5	26.7	270	13	Q9YH42	Q9YH42 brachydantio
21	335.5	26.4	246	13	Q8G375	Q8G375 phrynocephala
22	334.5	26.3	153	11	Q9CYL2	Q9CYL2 mus musculus
23	331.5	26.1	177	13	Q91BL2	Q91BL2 poephila gu
24	319	25.1	247	13	Q8G377	Q8G377 tylocotritlo
25	294.5	23.2	101	6	Q9T722	Q9T722 macaca fusc
26	293	23.1	324	13	Q9XY95	Q9XY95 lampetra fl
27	291	22.9	186	12	Q9J5D9	Q9J5D9 fowipox vir
28	242	19.1	52	6	Q9N1V4	Q9N1V4 equus caball
29	226	17.8	85	6	Q02790	Q02790 macropus fu
30	224	17.6	42	6	Q02802	Q02802 trichosurus
31	220	17.3	85	6	Q13114	Q13114 isodon mac
32	220	17.3	85	6	Q13122	Q13122 tarsipes ro
33	220	17.3	85	6	Q02795	Q02795 ornithorhyn
34	220	17.3	85	6	Q02798	Q02798 petaurus br
35	220	17.3	85	6	Q13104	Q13104 cercarctus
36	220	17.3	85	6	Q02792	Q02792 notoryctes
37	220	17.3	85	6	Q13105	Q13105 dasynotoides
38	220	17.3	85	6	Q02801	Q02801 tachylosau
39	219	17.2	85	6	Q02803	Q02803 trichosurus
40	211	16.6	42	6	Q02794	Q02794 ornithorhyn
41	209	16.5	42	6	Q02800	Q02800 tachylosau
42	178.5	14.1	186	6	Q9BFJ4	Q9BFJ4 lemur catra
43	178.5	14.1	186	11	Q9NWT1	Q9NWT1 castor cana
44	176.5	13.9	186	6	Q9BFJ7	Q9BFJ7 octotona hy
45	175	13.8	185	6	Q9BFK6	Q9BFK6 talpa alta

ALIGNMENTS

RESULT 1

Q9UKL8 PRELIMINARY; PRT; 241 AA.

AC Q9UKL8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Nerve growth factor B.

GN NGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99256269; PubMed=10322959;

RA Tong Y., Wang H., Chen W.;

RT "Cloning and sequencing of the gene for premature beta nerve growth factor."

RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Tong Y., Wang H.;

RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF150960; AAD55975.1; -

DR HSSP; P01139; 1BET.

DR InterPro; IPR02072; NGF.

DR Pfam; PF00243; NGF; 1.

DR PRINTS; PR00268; NGF.

DR ProDom; PD002052; NGF; 1.

DR SMART; SM00140; NGF; 1.

DR PROSITE; PS00248; NGF_1; 1.

DR PROSITE; PS00270; NGF_2; 1.

SO SEQUENCE 241 AA; 26959 MW; 619DFC5EB3BD671 CRC64;

Query Match 99.7%; Score 1266; DB 4; Length 241;

Best Local Similarity 99.6%; Pred. No. 8.3e-117;

Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
QY 241 A 241
DB 241 A 241

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RESULT 2

```

Q9P208 PRELIMINARY; PRT; 241 AA.
ID Q9P208
AC Q9P208
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 15, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kltano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037517; BAA90437.1; -.
DR HSBP; F01139; 18ET.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF.
DR PRINTS; PR00268; NGF.
DR Prodom; PD002052; NGF.
DR SMART; SM00140; NGF.1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR NON TER 241
SQ SEQUENCE 241 AA; 2698 MW; D531ED825D96C14 CRC64;

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Query Match 99.6%; Score 1265; DB 4; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1e-116;
 Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
QY 241 A 241
DB 241 A 241

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DB 241 A 241

RESULT 3

```

Q96P60 PRELIMINARY; PRT; 241 AA.
ID Q96P60
AC Q96P60
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411526; AAL05874.1; -.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF.1.
DR Prodom; PD002052; NGF.1.
DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
DR PROSITE; PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 2696 MW; 745216485C21E558 CRC64;

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Query Match 99.1%; Score 1258; DB 4; Length 241;
 Best Local Similarity 98.8%; Pred. No. 5.1e-116;
 Matches 238; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLESTQPPREAADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMWGDKTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTTHFVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240
QY 241 A 241
DB 241 A 241

```

RESULT 4

```

Q9N2F0 PRELIMINARY; PRT; 241 AA.
ID Q9N2F0
AC Q9N2F0
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCI_TaxID=9593;
RN (1)
RP SEQUENCE FROM N.A.
RA Kltano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037519; BAA90439.1; -.

```

DR HSP; P01139; 1BET.
DR InterPro; IP002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
FT NON TER 241 241
SQ SEQUENCE 241 AA; 26915 MW; 6F5AD163C84B34 CRC64;

Query Match 98.3%; Score 1249; DB 6; Length 241;
Best Local Similarity 98.8%; Pred. No. 4e-115;
Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 5

Q9NZP1 PRELIMINARY; PRT; 241 AA.
AC Q9NZP1
DT 01-OCT-2000 (TRENBLrel. 15; Created)
DT 01-OCT-2000 (TRENBLrel. 15; Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19; Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=CHIMP-220;
RA Kitano T., Kobayakawa H., Saitou N.,
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037518; BAA90438.1; -
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
FT NON TER 241 241
SQ SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match 98.3%; Score 1248; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 5e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60

DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 6

Q9NZB9 PRELIMINARY; PRT; 241 AA.
AC Q9NZB9
DT 01-OCT-2000 (TRENBLrel. 15; Created)
DT 01-OCT-2000 (TRENBLrel. 15; Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19; Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ORAN-UI;
RA Kitano T., Kobayakawa H., Saitou N.,
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037520; BAA90440.1; -
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
FT NON TER 241 241
SQ SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;

Query Match 98.2%; Score 1247; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 6.2e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFSSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSEFVCDVSVMGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 7

ID Q9N183 PRELIMINARY; PRT; 217 AA.

AC Q9N183; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Beta nerve growth factor (Fragment).
 OS Macaca fasciata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9542;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BL00D;
 RX MEDLINE=99270338; PubMed=10340513;
 RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
 RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys.";
 RL J. Comp. Neurol. 408:378-398 (1999).
 [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BL00D;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF222682; AAF3790.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF 1; 1.
 DR PROSITE; PS50270; NGF 2; 1.
 FT NON_TER
 FT 1 217
 SQ SEQUENCE 217 AA; 24240 MW; 36A5A2D1DFC8D5C CRC64;

Query Match 89.1%; Score 1132; DB 6; Length 217;
 Best Local Similarity 98.2%; Pred. No. 1.2e-103;
 Matches 213; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 AFIIGIOAEPHSESNVPAHTTIPQVHTKLOHSIDTLRRRSPAPAAIAARVAGQTRNI 70
 DB 1 AFIIGIOAEPHSESNVPAHTTIPQVHTKLOHSIDTLRRRSPAPAAIAARVAGQTRNI 60
 QY 71 TVDRLFKKRLRSRVLSTOPREAADTODLFEVGAAPFRTTRSKRSSHPFHR 130
 DB 61 TVDRLFKKRLRSRVLSTOPREAADTODLFEVGAAPFRTTRSKRSSHPFHR 120
 QY 131 GEFSVCDVSVMVDKTTATDIDIKGEVWLGVEVINNSVFKQVFFETKCDPENVDSGCR 190
 DB 121 GEFSVCDVSVMVDKTTATDIDIKGEVWLGVEVINNSVFKQVFFETKCDPENVDSGCR 180
 QY 191 GIDSKHNSYCTTHTTVKALTMGKQAAFRIRIDT 227
 DB 181 GIDSKHNSYCTTHTTVKALTMGKQAAFRIRIDT 217

RESULT 8

ID Q91XB4 PRELIMINARY; PRT; 294 AA.

AC Q91XB4; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Similar to nerve growth factor, beta.
 GN NGFB.
 MS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SALIVARY GLAND;
 RA Straube R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011123; AAH1123.1; -
 DR MGI; 97321; NGFb.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR PROSITE; PS00248; NGF 1; UNKNOWN_1.
 DR PROSITE; PS50270; NGF 2; 1.
 SQ SEQUENCE 294 AA; 32326 MW; 9EE7402DAC899229 CRC64;

Query Match 81.7%; Score 1038; DB 11; Length 294;
 Best Local Similarity 84.6%; Pred. No. 3.3e-94;
 Matches 193; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFIIGIOAEPHSESNVPAHTTIPQVHTKLOHSIDTLRRRSPAPAAIA 60
 DB 67 MSMLFYTLITAFIIGIOAEPHSESNVPAHTTIPQVHTKLOHSIDTLRRRSPAPAAIA 126
 QY 61 ARVAGQTRNTVDPRLFKKRLRSRVLSTOPREAADTODLFEVGAAPFRTTRSK 120
 DB 127 ARVAGQTRNTVDPRLFKKRLRSRVLSTOPREAADTODLFEVGAAPFRTTRSK 186
 QY 121 RSSSHPIFHGEFSVCDVSVMVDKTTATDIDIKGEVWLGVEVINNSVFKQVFFETKCR 180
 DB 187 RSSSHPIFHGEFSVCDVSVMVDKTTATDIDIKGEVWLGVEVINNSVFKQVFFETKCR 246
 QY 181 DPNVPDSCGKIDSKHNSYCTTHTTVKALTMGKQAAFRIRIDT 228
 DB 247 ASNPVDSGCRGIDSKHNSYCTTHTTVKALTMGKQAAFRIRIDT 294

RESULT 9

ID Q9DEZ9 PRELIMINARY; PRT; 241 AA.

AC Q9DEZ9; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Nerve growth factor.
 OS Crotales durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8732;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE=VENOM GLAND;
 RA Hayashi M.A.F., Radis-Baptista G., Yamane T., Camargo A.C.M.;
 RT "Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
 RT durissus terrificus) nerve growth factor.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF306533; AAG30924.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF 1; 1.
 DR PROSITE; PS50270; NGF 2; 1.
 SQ SEQUENCE 241 AA; 27116 MW; 4A261F42C5D6F3F CRC64;

Query Match 56.1%; Score 713; DB 13; Length 241;
 Best Local Similarity 59.8%; Pred. No. 3e-62;
 Matches 144; Conservative 29; Mismatches 58; Indels 10; Gaps 4;

QY 1 MSMLFYTLITAFILIGIOAEPHSESNVPAQ---HTIPQVHTKLQHSIDTALRRASAPA 56
 DB 1 MSMLCTLLIATLIGIWAAPKSESNVPLSGPATSDLSSTSCATHTALKTSMIDQHYPA 60
 QY 57 AAIYA-RVAGQTRNTIVDPPLFKKRLRSPRVLFSTOPPREAADTODLDEFGAAPPNR 115
 DB 61 PKAEBOEFGSANNIVDPPLFKRRFQSPRVLFSTQPPPLSRDEQSV---DANSINR 116
 QY 116 THRSKSSSHPIFRGEFSVCSVSWVWGKTATDICKGEVNLGEVINNSVFKQYFF 175
 DB 117 NIRAAR-EDHPHAKREYSVCSVSWVWANKTATDIGNLVTVWVDVNNNNVYKQYFF 175
 QY 176 ETKCRDPNVDSGCRGIDSKHNSYCTTHTFYKALTMDSQAAMPFIRIDTACVCLSR 235
 DB 176 ETKCRPNVPVPGCRGIDARHNSYCTTNTFYKALTMDSQAAMPFIRIDTACVCLSR 235
 QY 236 K 236
 DB 236 K 236

RESULT 10

Q90W38 PRELIMINARY; PRT; 241 AA.
 ID Q90W38;
 AC Q90W38;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative neurotrophic growth factor.
 GN NGF.
 OS Bothrops jararacussu (Jararacussu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 NC NCBI_TaxID=8726;
 RN [1]
 RS SEQUENCE FROM N.A.
 RA TISSUE=VENOM GLAND;
 RA Kaethim S., Pereira J.O., Astolfi Filho S., Soares A.M.,
 RA Cintra A.C.O., Giglio J.R., Franca S.C.;
 RT "Molecular cloning and cDNA sequence of a nerve growth factor
 precursor from Bothrops jararacussu venomous gland.";
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY007318; AAG12169.1;
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
 DR PROSITE; PS50270; NGF_2; 1.
 SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CRC64;

Query Match 55.8%; Score 709; DB 13; Length 241;
 Best Local Similarity 59.3%; Pred. No. 7,4e-62;
 Matches 143; Conservative 29; Mismatches 59; Indels 10; Gaps 4;

QY 1 MSMLFYTLITAFILIGIOAEPHSESNVPAQ---HTIPQVHTKLQHSIDTALRRASAPA 56
 DB 1 MSMLCTLLIATLIGIWAAPKSESNVPLSGPATSDLSSTSCATHTALKTSMIDQHYPA 60
 QY 57 AAIYA-RVAGQTRNTIVDPPLFKKRLRSPRVLFSTOPPREAADTODLDEFGAAPPNR 115
 DB 61 PKAEBOEFGSANNIVDPPLFKRRFQSPRVLFSTQPPPLSRDEQSV---DANSINR 116
 QY 116 THRSKSSSHPIFRGEFSVCSVSWVWGKTATDICKGEVNLGEVINNSVFKQYFF 175
 DB 117 NIRAAR-EDHPHAKREYSVCSVSWVWANKTATDIGNLVTVWVDVNNNNVYKQYFF 175
 QY 176 ETKCRDPNVDSGCRGIDSKHNSYCTTHTFYKALTMDSQAAMPFIRIDTACVCLSR 235
 DB 176 ETKCRPNVPVPGCRGIDARHNSYCTTNTFYKALTMDSQAAMPFIRIDTACVCLSR 235
 QY 236 K 236

DB 236 K 236

RESULT 11

Q9PTC3 PRELIMINARY; PRT; 87 AA.
 ID Q9PTC3;
 AC Q9PTC3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Beta nerve growth factor (Fragment).
 GN NGF.
 OS Cereus elaeagnus scotticus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Cervinae; Cervus.
 NC NCBI_TaxID=109627;
 RN [1]
 RS SEQUENCE FROM N.A.
 RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
 RA Suttle J.M.;
 RT "NGF expression in Antler.";
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF145043; AAF17235.1;
 DR HSP; P01139; IBBT.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON_TER 1
 FT NON_TER 87
 SQ SEQUENCE 87 AA; 9876 MW; 17EB06B49AF7A0A4 CRC64;

Query Match 36.4%; Score 462; DB 6; Length 87;
 Best Local Similarity 96.6%; Pred. No. 4.7e-38;
 Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 138 SVSWVWGKTATDICKGEVNLGEVINNSVFKQYFFETCRPNPVDSCRGIDSKHNS 197
 DB 1 SVSWVWGKTATDICKGEVNLGEVINNSVFKQYFFETCRPNPVDSCRGIDSKHNS 60
 QY 198 NSYCTTHTFYKALTMDSQAAMPFIR 224
 DB 61 NSYCTTHTFYKALTMDSQAAMPFIR 87

RESULT 12

Q9P2Z4 PRELIMINARY; PRT; 87 AA.
 ID Q9P2Z4;
 AC Q9P2Z4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Truncated beta nerve growth factor (Fragment).
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RS SEQUENCE FROM N.A.
 RA MEDLINE=95236507; PubMed=7720122;
 RA Li Y., Huang B., Cai L.;
 RT "Amplification, cloning and sequencing of beta nerve growth factor
 gene in the Chinese population.";
 RL Chung-Kuo I Hsueh Ko Hsueh Yuan Hsueh Pao 16:334-338(1994).
 DR EMBL; S76884; AAB34114.2;
 DR HSP; P01139; IBBT.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.

DR ProDom, PD002052, NGF, 1.
 DR SMART, SM00140, NGF, 1.
 DR PROSITE, PS0270, NGF 2, 1.
 FT NON TER 1
 SQ SEQUENCE 87 AA, 9729 MW, 45E9E27388FDEE27 CRC64;

Query Match
 Best Local Similarity 94.3%; Score 459; DB 4; Length 87;
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 122 SSSHIIFRGEFVSDSVWVGDTTATDIDKGEVWMLGEVINNSVFKYFFETKCRD 181
 DB 1 SSSHIIFRGEFVSDSVWVGDTTATDIDKGEVWMLGEVINNSVFEQYFETKCRD 60

QY 182 PNPVDSGCRGIDSKHMNSYCTTHREY 208
 DB 61 PNPVDSGCRGIDSKHMNSYCTTHREY 87

RESULT 13
 Q9WU15 PRELIMINARY; PRT; 132 AA.

DR 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Nerve growth factor (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansen H.T., Lehman M.N., Stevens P.J.;
 RT "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF104239; AAD21010.1; -
 FT NON TER 1
 FT NON TER 132
 SQ SEQUENCE 132 AA, 14649 MW, 0C36B6283225DA6 CRC64;

Query Match.
 Best Local Similarity 75.4%; Score 449.5; DB 11; Length 132;
 Matches 89; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKIQHSIDTALRRASAPAAIA 60
 DB 16 MSMLFYTLITAFILGIGQAEPTDSIVEGDSVPQAHWTKLQHSYDTALRRASAPASIA 75

QY 61 ARVAGOTRNTIVDRLFKKRLRSRVLFTSTOPREAADPQDDFEVGAAPRRTR 118
 DB 76 ARVAGOTRNT-GRQLFKKRLRSRVLFTSAQPPPTADTLDLDFQAGHTISFRKTR 132

RESULT 14
 Q9N182 PRELIMINARY; PRT; 241 AA.

DR 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Neurotrophin-3 (Fragment).
 OS Macaca fasciata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gotz R., Koster R., Winkler C., Raulf F., Lottepeich F., Scharf M.,
 RX MEDLINE=99270338; PubMed=10340513;
 Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys."
 RT J. Comp. Neurol. 408:378-398(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;
 RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
 RT their receptor messenger RNAs in monkey rhinal cortex."
 RL Neuroscience 0:0-0(2000).
 DR EMBL, AF222683; AAF33791.1; -
 DR HSSP; P20783; 1B8X
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 FT NON TER 1
 FT NON TER 241
 SQ SEQUENCE 241 AA, 27803 MW, AB95E457C7B07113 CRC64;

Query Match
 Best Local Similarity 33.6%; Score 426.5; DB 6; Length 241;
 Matches 97; Conservative 35; Mismatches 85; Indels 31; Gaps 6;

QY 4 LFYTLITAFILGIGQAEPSHSNVPAGHTIPQV-----HMTKLOHSLDTAL 48
 DB 1 LFYTLITAFILGIGQAEPSHSNVPAGHTIPQV-----HMTKLOHSLDTAL 60

QY 49 RRA-----RSAPAAIAARVAGOTRNTIVDRLFK-KRLRSRVLFTSTOPREAADT 100
 DB 61 PKAEPREPREGQPAKSEFQPV-----IAMDTELLRQGRVNSPRLTSDSPLEPPPL 114

QY 101 QDDFEVGAAPRRTRHRSRSSHPIFRGESVCDSDSVWVGDTTATDIDKGEVWML 160
 DB 115 YLMEDEVGNPVPANRSTRKRVAENK-SHREGVSDSSELTWTDSSALIDIGHQVTVL 173

QY 161 GEVINNSVFKYFFETKCRDPNPVDSGCRGIDSKHMNSYCTTHREYKALTYMD-GKQAA 219
 DB 174 GEIKTNSVYKQFYTRCKEARPVKNGCRGIDDKHMNSQCKTSQYVRLTSENKLVG 233

QY 220 WRFIRIDT 227
 DB 234 WRFIRIDT 241

RESULT 15
 Q91988 PRELIMINARY; PRT; 286 AA.

DR 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Neurotrophin-6 precursor.
 OS Xiphophorus maculatus (Southern platyfish), and
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 NCBI_TaxID=8083, 8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95059452; PubMed=7969471;
 RA Gotz R., Koster R., Winkler C., Raulf F., Lottepeich F., Scharf M.,
 RX "Neurotrophin-6 is a new member of the nerve growth factor family."
 Nature 372:266-269(1994).
 DR EMBL, L36942; AAA61923.1; -
 DR EMBL, L36325; AAA61922.1; -

DR EMBL; L36326; AAA61921.1; -
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR Signal.
KW SIGNAL.
FT CHAIN 1 142
SQ SEQUENCE 286 AA; 31424 MW; 5607DBA66792E12D CRC64;
NEUROTROPHIN-6.
Query Match 33.5%; Score 426; DB 13; Length 286;
Best Local Similarity 38.6%; Pred. No. 7.5e-34;
Matches 110; Conservative 31; Mismatches 84; Indels 60; Gaps 10;
QY 8 LITAFLLIGIOAEPPHSESNV-----PAGHTIPQVH-----WTKLQHSIDTALRA 51
DB 6 LVLLLLIGVQAVLNMGGLARNPGAAHNSAGQETAAARGQLSODQTSYQOHRTHRTK 65
QY 52 RSAPAAA-----IAARVAGQT---RNIIVDPRLFKRRRLR-SPRVLFs-TPPREAA 98
DB 66 RTQSAASNMQNRTPVIGSPAGSSPDPSVPVDPKLFSGKHTRPSPRVFSEVIPSMDVL 125
QY 99 DTQDIDFE-VGGADPFNRTNRSKRSSSHPIFRGEPSCDSVSVWVGDKTTATDIKKEV 157
DB 126 DQEGYDFERVRGL-----RVRRKAVSHMVRGYSVCDsINTWV-NKTRATDMsGNEV 177
QY 158 MYLGEVNNINSVFQYFPETKCRD-----NEVDSGCRGIDSK 195
DB 178 TVLSHVIVNNKVKQLFEYETCRSPTHRSSGIVIGRSGGRGKQSKTGNSGCRGIDSR 237
QY 196 HMNSYCTTHTFEVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
DB 238 YMNSHCTNTDIYSALIVFKEQTAFIRINAAVCVLSRNSWSR 282

Search completed: June 6, 2003, 10:50:56
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:02 / Search time 9 Seconds

(without alignments)
1110.644 Million cell updates/sec

Title: US-09-788-188-1
Perfect score: 1270
Sequence: 1 MSMLFYTLIFALIGIOAEP.....FIRIDTACVLSRAVRA 241

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1270	100.0	241	1	NGF_HUMAN
2	1124	88.5	229	1	NGF_PIG
3	1107	87.2	241	1	NGF_RAT
4	1106	87.1	231	1	NGF_BOVIN
5	1096	86.3	241	1	NGF_MOUSE
6	1092	86.0	241	1	NGF_MOUSE
7	1073	84.5	241	1	NGF_CAVPO
8	788.5	62.1	243	1	NGF_PRANA
9	773	60.9	231	1	NGF_CHICK
10	675.5	53.2	243	1	NGF_XENLA
11	484	38.1	117	1	NGF_DABNR
12	481.5	37.9	114	1	NGF_XIPWA
13	481.5	37.9	257	1	NT3_HUMAN
14	474	37.3	260	1	NT3_XENLA
15	473.5	37.3	257	1	NT3_XENLA
16	472	37.2	258	1	NT3_MOUSE
17	471.5	37.1	257	1	NT3_CHICK
18	471	37.1	258	1	NT3_RAT
19	459.5	36.2	233	1	NT7_BRABE
20	449.5	35.4	116	1	NGF_NAJNA
21	445.5	35.1	116	1	NGF_NAJNA
22	372.5	29.3	140	1	NT7_CYPCA
23	365	28.7	247	1	BDNF_HUMAN
24	364	28.7	249	1	BDNF_RAT
25	363	28.6	255	1	BDNF_CAVPO
26	362	28.5	247	1	BDNF_PROLO
27	361	28.4	247	1	BDNF_URSAR
28	361	28.4	249	1	BDNF_URSAR
29	360	28.3	249	1	BDNF_MOUSE
30	358.5	28.2	247	1	BDNF_PIG
31	350	27.6	247	1	BDNF_FELCA
32	348.5	27.4	248	1	BDNF_BOVIN
33	347.5	27.4	246	1	BDNF_CHICK

34	343	27.0	236	1	NT4_XENLA	P24727 xenopus lae
35	338.5	26.7	270	1	BDNF_CYPCA	Q90322 cyprinus ca
36	337.5	26.6	210	1	NT5_HUMAN	P34130 homo sapien
37	335	26.4	269	1	BDNF_XIPWA	Q02193 xiphophorus
38	330.5	26.0	209	1	NT5_RAT	P34131 rattus norv
39	323.5	25.5	114	1	BDNF_MACMU	O06225 macaca mla
40	307.5	24.2	114	1	BDNF_XENLA	P25432 xenopus lae
41	230	18.1	257	1	NT6B_HUMAN	P34133 homo sapien
42	227	17.9	257	1	NT6A_HUMAN	P34132 homo sapien
43	225	17.7	186	1	NT6G_HUMAN	P34134 homo sapien
44	190	15.0	42	1	NGF_VIPLE	P25428 vipera lebe
45	136	10.7	154	1	NT3_CEREL	Q95150 cervus elap

ALIGNMENTS

RESULT 1
NGF_HUMAN STANDARD, PRT, 241 AA.
AC P01138;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83244969; PubMed=668123;
RA Ullrich A., Gray A., Berman C., Dull T.J.;
RT "Human beta-nerve growth factor gene sequence highly homologous to
RL that of mouse.";
RL Nature 303:821-825(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84206565; PubMed=6327169;
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
RT "Sequence homology of human and mouse beta-NGF subunit genes.";
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=90326556; PubMed=2374737;
RA Borsani G., Pizanti A., Rugaril E.I., Falini A., Silani V.,
RT "cDNA sequence of human beta-NGF.";
RL Nucleic Acids Res. 18:4020-4020(1990).
RN [4]
RP SEQUENCE OF 178-219 FROM N.A.
RC TISSUE=Leukocyte; PubMed=2025430;
RX MEDLINE=9122573; PubMed=2025430;
RA Halboeck F., Ibanez C.F., Petersen H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC EMBL; V01511; CA24755.1; -
DR EMBL; M21062; AA5931.1; -
DR EMBL; X52599; CA36832.1; -
DR PIR; A01399; NGHEM.
DR PIR; S10253; S10253.
DR HSSP; P01139; 1BET.
DR GenBank; HGNC; 7808; NGFB.
DR MIM; 162030; -
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP.
FT CHAIN.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT CARBOHYD.
FT CARBOHYD.
SQ SEQUENCE 241 AA; 26987 MW; CFI84DC6B736B0F CRC64;

Query Match 100.0%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLLITAPLIGIOAEPSHSNVPAGHTIPQVHNTKLOHSLDTRARASAPAAIA 60
DB 1 MSMLFYLLITAPLIGIOAEPSHSNVPAGHTIPQVHNTKLOHSLDTRARASAPAAIA 60
QY 61 ARVAGQRRNTVDPRLFKKRLSPRLFSTQPPREADODDPEVGAAPRRTRSK 120
DB 61 ARVAGQRRNTVDPRLFKKRLSPRLFSTQPPREADODDPEVGAAPRRTRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQFFETKCR 180
QY 181 DENPVDSGCRGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAVR 240
DB 181 DENPVDSGCRGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 2
NGF_PIG STANDARD; PRT; 229 AA.
ID NGF_PIG
AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
(1)
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RX MEDLINE=9431891; PubMed=8039422;
RA Lab1bD-nanale Y.; Mellink C.; Yeste M.; Gellin J.;
RT A new marker (NGFB) on pig chromosome 4, isolated by using a
RT consensus sequence conserved among species.
RL Cytogenet. Cell Genet. 67:120-125 (1994).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC
DR EMBL; L31898; AAA21301.1; -
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP.
FT CHAIN.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT CARBOHYD.
FT CARBOHYD.
SQ SEQUENCE 229 AA; 25275 MW; FE8890771CBA3189 CRC64;

Query Match 88.5%; Score 1124; DB 1; Length 229;
Best Local Similarity 92.6%; Pred. No. 2e-99;
Matches 212; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 13 LIGIOAEPSHSNVPAGHTIPQVHNTKLOHSLDTRARASAPAAIAARVAGQRRNTV 72
DB 1 LIGIOAEPSHSNVPAGHTIPQVHNTKLOHSLDTRARASAPAAIAARVAGQRRNTV 72
QY 181 DENPVDSGCRGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAVR 241
DB 181 DENPVDSGCRGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRAVR 241
QY 241 A 241
DB 241 A 241

RESULT 3
NGF_PAT STANDARD; PRT; 241 AA.
ID NGF_PAT
AC P25427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=3184206;

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Db      1 MSMLFYTLITAFLLIGVQAEPTDTSNVEGDSVPEAHMTKLQHSIDTALRRRARSAPATAPIA 60
Qy      61 ARVAGGTNRNTVDPRLFKKRLRSRVLVSTOFPREAAOTODIDREVGAAAPNRTRRSK 120
Db      61 ARVAGGTNRNTVDPRLFKKRLRSRVLVSTOFPREAAOTODIDREVGAAAPNRTRRSK 120
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Qy      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240

RESULT 6
NGF_CAVPO STANDARD; PRT; 241 AA.
ID NGF_CAVPO
AC P19093;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
OS NGFB.
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OC NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Prostate;
RX MEDLINE=89177243; PubMed=2926397;
RA Schwarz M.A., Fisher D., Bradshaw R.A., Isaacson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
RL from the guinea pig prostate gland."
J. Neurochem. 52:1203-1209(1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR, J10097; J10097.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 229
FT CARBOHYD 189
FT CARBOHYD 231
FT CARBOHYD 69
FT CARBOHYD 114
FT CARBOHYD 114
FT SEQUENCE 241 AA; 26821 MW; 2FAE26B197804BF4 CRC64;

Query Match 86.0%; Score 1092; DB 1; Length 241;
Best Local Similarity 86.2%; Pred. No. 2,3e-96;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

Qy      1 MSMLFYTLITAFLLIGVQAEPTDTSNVEGDSVPEAHMTKLQHSIDTALRRRARSAPATAPIA 60
Db      1 MSMLFYTLITAFLLIGVQAEPTDTSNVEGDSVPEAHMTKLQHSIDTALRRRARSAPATAPIA 60
Qy      61 ARVAGGTNRNTVDPRLFKKRLRSRVLVSTOFPREAAOTODIDREVGAAAPNRTRRSK 120
Db      61 ARVAGGTNRNTVDPRLFKKRLRSRVLVSTOFPREAAOTODIDREVGAAAPNRTRRSK 120
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Qy      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240

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Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Db      122 RSTHPVFMGERSVCDVSVMVGDKTATADIKGEVMVLGEVNNINSVPKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Qy      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240
Db      181 ASPVDSGCRGIDSKHMSYCTTHTFVATLMDGQOAMRFRIDTACVCLSRKAVR 240

RESULT 7
NGF_PRANA STANDARD; PRT; 241 AA.
ID NGF_PRANA
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
OS NGFB.
OC Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OC NCBI_TaxId=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89172070; PubMed=3234767;
RA Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
RL precursor from Mastomys natalensis."
Gene 63:257-264(1988).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; M22748; AAA40599.1; ALT_INT.
DR PIR; J03433; NGRTBA.
DR HSSP; P01139; 1BETG.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 229
FT CARBOHYD 189
FT CARBOHYD 231
FT CARBOHYD 69
FT CARBOHYD 114
FT CARBOHYD 114
FT SEQUENCE 241 AA; 27035 MW; 8BFB207A1FEB27 CRC64;

Query Match 84.5%; Score 1073; DB 1; Length 241;
Best Local Similarity 83.3%; Pred. No. 1.5e-94;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy      1 MSMLFYTLITAFLLIGVQAEPTDTSNVEGDSVPEAHMTKLQHSIDTALRRRARSAPATAPIA 60
Db      1 MSMLFYTLITAFLLIGVQAEPTDTSNVEGDSVPEAHMTKLQHSIDTALRRRARSAPATAPIA 60

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Db 1 MSMLFTLITALLIGVQAPYDSDNLPEDSDVPEANWTLQHSIDTLRLRRASAPAPA 60
Qy 61 ARVAGGTNTITDPLFKKRLRSRVLFTSTOPPEADTODLDFEVGAAFPNTRRSK 120
Db 61 ARVAGGTNTITDPLFKKRLRSRVLFTSTOPPEADTODLDFEVGAAFPNTRRSK 120
Qy 121 RSSSHIFRHSSEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFKQYFETKCR 180
Db 121 RSSSHIFRHSSEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFKQYFETKCR 180
Qy 121 RSSSHIFRHSSEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFKQYFETKCR 180
Db 121 RSSSHIFRHSSEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFKQYFETKCR 180
Qy 181 DPNPVDGCGRIDSKMNSYCTTHTFVALTMGKQAMRFRIDTACVLSKRAVR 240
Db 181 ANNPVSSGCGRIDSKMNSYCTTHTFVALTMGKQAMRFRIDTACVLSKRAVR 240

RESULT 8
NGF CHICK STANDARD; PRT; 243 AA.
AC P05200;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1]
RX SEQUENCE FROM N.A.
RA MEDLINE=86300646; PubMed=3017695;
RA Ebdendahl T., Larhammar D., Persson H.;
RA "Structure and expression of the chicken beta nerve growth factor
RT gene.";
RL EMO J. 5:1483-1487(1986).
RN 2]
RX SEQUENCE OF 118-243 FROM N.A.
RA MEDLINE=86248129; PubMed=3720959;
RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
RA Auffray C.;
RA "Molecular cloning of the avian beta-nerve growth factor gene:
RT transcription in brain.";
RL PERS Lett. 203:82-86(1986).
RN 3]
RX SEQUENCE OF 121-243 FROM N.A.
RA MEDLINE=86300647; PubMed=2427334;
RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RA "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMO J. 5:1489-1493(1986).
RN 4]
RX SEQUENCE OF 181-222 FROM N.A.
RA MEDLINE=91223573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RA "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC DR EMBL; X04003; CAA27633.1; ALT_INIT.
CC DR EMBL; X04067; CAA27703.1;
CC DR EMBL; M26810; AAA48984.1;
CC DR PIR; A24857; A24857.
CC DR PIR; A26311; A26311.
CC DR HSSP; P01139; 1BET.
CC DR InterPro; IPR002072; NGF.
CC DR Pfam; PF00243; NGF; 1.
CC DR PRINTS; PR00268; NGF.
CC DR PRODOM; PD002052; NGF; 1.
CC DR SMART; SM00140; NGF; 1.
CC DR PROSITE; PS00248; NGF; 1; 1.
CC DR PROSITE; PS0270; NGF; 2; 1.
CC KM Growth factor; Signal.
CC FT SIGNAL 1 22
CC FT PROPER 23 125
CC FT CHAIN 126 243
CC FT DISULFID 139 204
CC FT DISULFID 182 232
CC FT DISULFID 192 234
CC SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 62.1%; Score 788.5; DB 1; Length 243;
Best Local Similarity 64.9%; Pred. No. 1,46-67;
Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;

Qy 1 MSMLFTLITALLIGVQAPYDSDNLPEDSDVPEANWTLQHSIDTLRLRRASAPAPA 56
Db 5 MSMLYTLITALLIGVQAPYDSDNLPEDSDVPEANWTLQHSIDTLRLRRASAPAPA 57
Qy 57 AAIARVA-----GQNTITVDPRLFKKRLRSRVLFTSTOPPEADTODLDFEVGAA 111
Db 58 TT-HGRANMPDGDIEDINIMDQNFKKRFRSRVLFTSTOPPEVSKGSTGF-LSSAV 115
Qy 112 PPNRTRSKSSSHPIFRHSSEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFK 171
Db 116 SLNRRTATKTA-TAPVLRHGEFVSDSVWVGDKTATDICKKXVWVLGEVININNSVFK 174
Qy 172 QYFETKCRPNVDSGCGRIDSKMNSYCTTHTFVALTMGKQAMRFRIDTACVC 231
Db 175 QYFETKCRPNVDSGCGRIDSKMNSYCTTHTFVALTMGKQAMRFRIDTACVC 234
Qy 232 VLSRKAVR 239
Db 235 VLSRKSGR 242

RESULT 9
NGF XENLA STANDARD; PRT; 231 AA.
ID NGF XENLA
AC P1617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DB Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 1]
RX SEQUENCE FROM N.A.
RA MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campion M., Cardinali B., Pierandrei-Amaldi P.;
RA "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos.";
RL Mol. Reprod. Dev. 29:313-322(1991).
RN 2]
RX SEQUENCE OF 170-211 FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE=91222573; PubMed=2025430;

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RA Halboeck F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.";
 CC Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SYMPATHETIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL: X55716; CAA39249.1; ALT_INIT.
 CC PIR: S1481; S1481.
 CC DR HSSE, P01139; 1BET.
 CC DR InterPro: IPR002072; NGF.
 CC Pfam: PF00243; NGF; 1.
 CC DR PRINTS: PR00268; NGF.
 CC DR ProDom: PD002052; NGF; 1.
 CC DR SMART: SM00140; NGF; 1.
 CC DR PROSITE: PS00248; NGF 1; 1.
 CC DR PROSITE: PS02070; NGF 2; 1.
 CC DR Growth factor; signal.
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 114 POTENTIAL.
 CC FT CHAIN 115 231 NERVE GROWTH FACTOR.
 CC FT DISULFID 128 193 BY SIMILARITY.
 CC FT DISULFID 171 221 BY SIMILARITY.
 CC FT DISULFID 181 223 BY SIMILARITY.
 CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;
 CC -----
 CC Query Match 60.9%; Score 773; DB 1; Length 231;
 CC Best Local Similarity 63.6%; Pred. No. 3.9e-66;
 CC Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;
 CC 1 MSMLFTLITLFLIGIOAEPHSNSVPAHGT---IP-QVHWTK-LQHSIDLALRRASA 54
 CC 1 MSMLFTLITLILISVQAAPKTKDAPARSSAKSRIPHTHTKSLHNS----- 49
 CC 55 PAAAIARVAQOTRNTVDPRLFKKRLRSPRVLPSTOPPREADOTDLDPEVGAAPFN 114
 CC 50 -HGKLEAKPEPYSFNNVTDPKLFRKRPSPRVLPSTOPPLSEDFQHLLEY-LDDEBSLN 107
 CC 115 RTHSKSSSHPIFRGGEFVSVDISVWVGDKTATDTDKGKEMVLGKVNINNSVFKQYF 174
 CC 108 KTRAKR-TYAPVHKGEYSVCDISVMWVGKTKATDKGKEVTYLGKVNINNSVFKQYF 166
 CC 175 FETCRDPNPVDSGGRGIDSKHMNSYCTTHTFVALTMDGKQAAWRIRIDTACVLSR 234
 CC 167 FETCRDPNPVDSGGRGIDSKHMNSYCTTHTFVALTMDGKQAAWRIRIDTACVLSR 226
 CC 235 RK 236
 CC 227 RK 228
 CC -----
 CC RESULT 10
 CC NGF_BUNMU STANDARD; PRT; 243 AA.
 CC AC P34128;
 CC DT 01-FEB-1994 (Rel. 28, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 CC NCBI_Taxid=8616;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Venom gland;
 CC RX MEDLINE=93192074; PubMed=7916740;
 CC RA Dane J.M.; Garner J.M.;
 CC RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor
 CC from the krait, Bungarus multicinctus.";
 CC Growth factors 8:77-86(1993).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SYMPATHETIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: S56212; AAB25729.1; -
 CC DR HSSE, P01139; 1BET.
 CC DR InterPro: IPR002072; NGF.
 CC Pfam: PF00243; NGF; 1.
 CC DR PRINTS: PR00268; NGF.
 CC DR ProDom: PD002052; NGF; 1.
 CC DR SMART: SM00140; NGF; 1.
 CC DR PROSITE: PS00248; NGF 1; 1.
 CC DR PROSITE: PS02070; NGF 2; 1.
 CC DR Growth factor; signal.
 CC FT SIGNAL 1 18 POTENTIAL.
 CC FT PROPEP 19 125 NERVE GROWTH FACTOR.
 CC FT CHAIN 126 243 BY SIMILARITY.
 CC FT DISULFID 139 204 BY SIMILARITY.
 CC FT DISULFID 182 232 BY SIMILARITY.
 CC FT DISULFID 192 234 BY SIMILARITY.
 CC SQ SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;
 CC -----
 CC Query Match 53.2%; Score 675.5; DB 1; Length 243;
 CC Best Local Similarity 56.8%; Pred. No. 7.3e-57;
 CC Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;
 CC 1 MSMLFTLITLFLIGIOAEPHSNSVPAHGT---HTIQVHWTKLQHSIDLALRRASA 56
 CC 1 MSMLFTLITLILISVQAAPKTKDAPARSSAKSRIPHTHTKSLHNS----- 49
 CC 57 AAIARVAQOTRNTVDPRLFKKRLRSPRVLPSTOPPREADOTDLDPEVGAAPFN 115
 CC 61 PKESDDELGAANITVDPKLFQRRFOSPRVLPSTOPPLSRQGVKFLQTEDTLNR 119
 CC 116 THRSKSSSHPIFRGGEFVSVDISVWVGDKTATDTDKGKEMVLGKVNINNSVFKQYF 175
 CC 120 NIMA-NMENHVNHGSHSVCDISVWVTKTKATDKGKEVTYLGKVNINNSVFKQYF 178
 CC 176 FETCRDPNPVDSGGRGIDSKHMNSYCTTHTFVALTMDGKQAAWRIRIDTACVLSR 235
 CC 179 FETCRDPNPVDSGGRGIDSKHMNSYCTTHTFVALTMDGKQAAWRIRIDTACVLSR 238
 CC 236 K 236
 CC 239 K 239

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RESULT 11
NGF_DABRR
ID NGF_DABRR STANDARD; PRT; 117 AA.
AC P30894;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF)
OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Daboia.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC TISUB=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
RT the venom of Vipera russelli russelli."
RL Biochim. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC PIR, S28161; S28161.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF; 1.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1;
DR PROSITE; PS50270; NGF; 2; 1.
KM Glycoprotein; Growth Factor.
FT DISULFID 12 77
FT DISULFID 55 105
FT DISULFID 65 107
FT CARBOHYD 21 21
SQ SEQUENCE 117 AA; 13283 MW; A64559CSEPCIF66 CRC64;

Query Match 38.1%; Score 484; DB 1; Length 117;
Best Local Similarity 74.1%; Pred. No. 4,4e-39;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 125 HPIFHREFSVCSVWVDKKTATDICKKENVVLGEVNNINSVFQYFFETKCRDNP 184
DB 1 HPVHNOQSEFVCSVSWVANKTATDITMRGAVTVWVDVNLNNVYKQYFFETKCRKNPN 60

QY 185 VDSGCRGIDSKHNSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSRK 236
DB 61 VPSGCRGIDAKHNSYCTTIDTFRALTLMERNOASMRFFINHTACVCLSRK 112

RESULT 12
NGF_XIPMA
ID NGF_XIPMA STANDARD; PRT; 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF)
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Petromorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.

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EX MEDLINE=92333301; PubMed=1629719;
RA Gotz R., Raulf F., Scharl M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
RT structure and function than nerve growth factor during vertebrate
RT evolution."
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X59941; CA442566.1; -
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1; FALSE_NEG.
DR PROSITE; PS50270; NGF; 2; 1.
KM Growth factor; Signal.
FT SIGNAL 1 30
FT PROPEP 31 79
FT CHAIN 80 194
FT DISULFID 90 155
FT DISULFID 133 183
FT DISULFID 143 185
SQ SEQUENCE 194 AA; 21596 MW; 0369E0FA51147AE CRC64;

Query Match 37.9%; Score 481.5; DB 1; Length 194;
Best Local Similarity 58.9%; Pred. No. 1,4e-38;
Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

QY 71 TYDPRLFKRRRLSPVLFSTOPEAADTODLDFE-VGGAAPFNTHSKRSSHPHF 129
DB 40 TYDPRLFKRRRLSPVLFSSQPP-----DAEPAGQGVSRKTRQPQ-----H 83

QY 130 RGEFSVCSVSWVVDKKTATDICKKENVVLGEVNNINSVFQYFFETKCRDNPVDSGC 189
DB 84 RGVSVCSVSWVGNKTVATDISKEVTVLPVNNINNVKKQYFFETTHCHSPSGSRC 143

QY 190 RIGDSKHNNSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSRK 237
DB 144 LGIDAHNNSHCTNSHTFVRLTSSENOVAWMLIRINACVCLSRKS 191

RESULT 13
NT3_HUMAN
ID NT3_HUMAN STANDARD; PRT; 257 AA.
AC P20783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
OS (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=90262727; PubMed=2344409;
 RA Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Laramie G.R., Nikolic K., Winslow J.W.,
 RA "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773 (1990).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045937; PubMed=2236018;
 RA Jones K.R., Reichardt L.F.,
 RA "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064 (1990).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90306351; PubMed=2365067;
 RA Kishino Y., Yoshimura K., Nakahama K.,
 RA "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RL FEBS Lett. 266:187-191 (1990).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91365361; PubMed=1869806;
 RA Maisongier P.C., le Beau M.M., Espinosa R. III, Ip N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.,
 RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RL Genomics 10:558-568 (1991).
 [5]
 RP SEQUENCE OF 194-236 FROM N.A.
 RX TISSUE=Leukocyte; PubMed=2025430;
 RA MEDLINE=91222573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.,
 RA "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858 (1991).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=95217877; PubMed=7703225;
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.,
 RA "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146 (1995).
 [7]
 RP VARIANT GLU-76.
 RX MEDLINE=95251647; PubMed=7733919;
 RA Hattori M., Nanko S.,
 RA "Association of neurotrophin-3 gene variant with severe forms of
 RT schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518 (1995).
 [8]
 RP VARIANT GLU-76.
 RX MEDLINE=96253892; PubMed=8925252;
 RA Arinami T., Takekoshi K., Itokawa M., Hamaguchi H., Toru M.,
 RA "Failure to find associations of the CA repeat polymorphism in the
 RT first intron and the Gln-63/Glu-63 polymorphism of the neurotrophin-3
 RL gene with schizophrenia.";
 RL Psychiatr. Genet. 6:13-15 (1996).
 [9]
 RP FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND
 PROPRIOCEPTIVE SENSORY NEURONS.
 [10]
 RP SUBCELLULAR LOCATION: Secreted.
 [11]
 RP TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 [12]
 RP POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 thought to be associated with severe forms of schizophrenia. This
 does not seem to be the case.
 [13]
 RP SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 [14]
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 CC
 DR EMBL; X53655; CA37703.1; -
 DR EMBL; M37763; AAA59953.1; -
 DR EMBL; M61180; AAA63231.1; -
 DR PIR; JH0141; JH0141.
 DR PIR; A36208; A36208.
 DR PIR; S10719; S10719.
 DR PIR; C40304; C40304.
 DR PDB; 1BND; 04-APR-96.
 DR PDB; 1B8K; 09-FEB-99.
 DR Genew; HGNC:8023; NTF3.
 DR MIM; 162660; -
 DR InterPro; IPR002400; GF_cysknct.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF_1.
 DR PRINTS; PR00438; GFCYSKNCT.
 DR PRINTS; PR00268; NGF.
 DR Prodom; PD002052; NGF_1.
 DR SMART; SM00140; NGF_1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS02070; NGF_2; 1.
 KW Growth factor; Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 16
 FT PROPEP 17 128
 FT CHAIN 139 257
 FT DISULFID 152 217
 FT DISULFID 195 246
 FT DISULFID 205 248
 FT CARBOHYD 131 131
 FT VARIANT 76 76
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT G->E.
 FT /FTID=VAR_012084.
 SQ SEQUENCE 257 AA; 29354 MW; 39A5BB3B28E25E03 CRC64;
 Query Match 37.9%; Score 481.5; DB 1; Length 257;
 Best Local Similarity 40.7%; Pred. No. 2e-38; Mismatches 88; Indels 31; Gaps 6;
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;
 QY 1 MSMTFTTLTFLVFLGIQAPHSSENVPAHGHTIPQV-----HWTKLQSLD 45
 DB 1 MSILFYVFLAVLRGIQNMNDQRLPEDSLNLIKIQADILKNTSKQNVDPKENVQ 60
 QY 46 TALRA-----RSAPAAIAARVAGQTNITWDPLFK-KRLRSRVLFSTQPPREA 97
 DB 61 STLPFAERPREPERGPKXSAFOPV-----IAMDTELRQORRNPSRVLISDTPLEP 114
 QY 98 ADTQDPEVGGAAPFNRTHSKRSSHPFRGRGFSVCSVWVGDKTATDIXKEV 157
 DB 115 PPLVIMEDYVSPVYVANTSRKRYAEK-SHREGYSVCSESLMVTDKSSAIDIRHQV 173
 QY 158 MYLGEVINNSVFRQYFEETKCRDPNPVSGRGISDKMNSYCTTTTFYKALTMQ-GK 216
 DB 174 TVLGEIKTNGSPVQYFEETKCRARPVKNGCRISIDKHMNSCKTSQTYRALTSNNK 233
 QY 217 QAAKFTITDPACTVLSRKAIVR 239
 DB 234 LVGWRWIRIDTSVCALSRKIGR 256
 RESULT 14
 ID NT3_XENLA STANDARD, PRT, 260 AA.
 AC P25435;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve
 OS growth factor 2) (NGF-2).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 CC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97252639; PubMed=9096131;
 RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
 RT Activity-dependent expression of NT-3 in muscle cells in culture:
 RL implications in the development of neuromuscular junctions.";
 RN J. Neurosci. 17:2947-2958(1997).
 RN [2]
 RP SEQUENCE OF 197-217 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91222573; PubMed=2025430;
 RA Halboeck F., Ibanez C.F., Persson R.;
 RT Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.";
 RN Neuron 6:845-858(1991).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL, U27576; AAB17723.1; -
 DR HSSP, P20783; 1B8X.
 DR InterPro, IPR002400; GF_cyknot.
 DR InterPro, IPR002672; NGF.
 DR Pfam, PF00243; NGF; 1.
 DR PRINTS; PR00438; GFCYSXNOT.
 DR PRINTS; PR00268; NGF.
 DR ProDom, PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 DR Growth factor; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 141
 FT CHAIN 142 260
 FT DISULFID 155 220
 FT DISULFID 198 249
 FT DISULFID 208 251
 FT CARBOHYD 134 134
 SQ SEQUENCE 260 AA; 30022 MW; FFB507A5EA33C65 CRC64;
 Query Match 37.3%; Score 474; DB 1; Length 260;
 Best Local Similarity 41.5%; Pred. No. 1e-37;
 Matches 108; Conservative 36; Mismatches 94; Indels 22; Gaps 7;
 Oy 1 MSMLFTLLTALFLIGQAEHSESNVPAH-----ITPVHMTK---LQSLDTALARRA 51
 Db 1 MSILFTVFLPYLLGSHATNDKKNLPENSNLSPIKLIQADILKKNISKQTVTKENHQ 60
 Oy 52 RSAPAAIAARVAGQTRN-----ITVDPLF---KKRLRSPRVLFSTOPPREADTQ 101
 Db 61 STPKPQLLDLDDDMKKDQFQVVISLALVQCKQRKRSRVLSDSLPPPLLYM 120
 Oy 102 DLDEVGGAAPF-NRTHRSKRSSSHPIFRGSEFVCDVSVMVGDKTATDICKKEVMVL 160
 Db 121 LMDYVIGSTVNNRSTRKRFAEHR-GHRGEYSVCSESLMTVDKNALDIRGHQTVL 179
 Oy 161 GEVAINSVKQYFETKCRDPNPVDSGCGIDSKHNSYVTTHTYVAKLMD-GKQAA 219
 Db 180 GEITGNSPVKQYFETKCRKARPVKNGCGRIDHWNSSQCKTSQTVRALTSENKMG 239
 Oy 220 WRFRIDTACVCLSRKAVR 239

DB 240 WRFRIDTSCVCLSRKIGR 259
 RESULT 15
 ID NT3_FELCA STANDARD; PRT; 257 AA.
 AC 09ST2;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
 DE (Nerve growth factor 2) (NGF-2).
 GN NT3.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felle.
 OC NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20211727; PubMed=10745216;
 RA Lein E.S., Hohn A., Shatz C.J.;
 RT "Dynamic regulation of BDNF and NT-3 expression during visual system
 RL development".
 RL J. Comp. Neurol. 420:1-18(2000).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL, AF192538; AAF03424.1; -
 DR HSSP, P20783; 1B8X.
 DR InterPro, IPR002072; NGF.
 DR Pfam, PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom, PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 DR Growth factor; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 138
 FT CHAIN 139 257
 FT DISULFID 152 217
 FT DISULFID 195 246
 FT DISULFID 205 248
 FT CARBOHYD 131 131
 SQ SEQUENCE 257 AA; 29403 MW; EB53F7E59C511B4 CRC64;
 Query Match 37.3%; Score 473.5; DB 1; Length 257;
 Best Local Similarity 40.1%; Pred. No. 1e-37;
 Matches 103; Conservative 40; Mismatches 95; Indels 19; Gaps 5;
 Oy 1 MSMLFTLLTALFLIGQAEHSESNVPAHTIPV-----HMTKLQSLD 45
 Db 1 MSILFTVIFLAYLRGIGNNMDQSRSLPDSINSLIKLIQADILKKNLSKQVLDKENYQ 60
 Oy 46 TARRARSAAPAAIAARVAGQTNIF-VDPRLFK-KRRLRSPRVLFSTOPPREADTQD 103
 Db 61 STPKKAPRREPQGPASBPQVPMDELRRQRRSSPVLSDSTPLPPPLLYM 120
 Oy 104 DFEVGAAPFNTRTHRSKRSSSHPIFRGSEFVCDVSVMVGDKTATDICKKEVMVL 163
 Db 121 EDVVGSPVAAKRSRKRFAEHR-SHRGEYSVCDSESLMTVDKSAIDIRGHQTVLGEI 179
 Oy 164 NINNSVFKQYFETKCRDPNPVDSGCGIDSKHNSYCTTHTYVAKLMD-GKQAAWR 222

Db 180 KSGNSPVKQYFETRCCKARPVKNCGCGIDDKEMNSQCTTSQTYVRALTSBNNKLVGMW 239

Qy 223 IRIDTACVCLSRKAVR 239

Db 240 IRIDTSCVCLSRKIGR 256

Search completed: June 6, 2003, 10:49:54
Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:52 ; Search time 15 Seconds

(without alignments)
1544.560 Million cell updates/sec

Title: US-09-788-188-1

Perfect score: 1270
Sequence: 1 MSMLFYTLITAFILIGIOAEP.....FIRIDTACVCVSRRAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1270	100.0	286	1 NCHUDM	nerve growth facto
2	1124	88.5	229	2 146614	nerve growth facto
3	1107	87.2	245	2 156570	nerve growth facto
4	1096	86.3	307	1 NGMSWG	beta-nerve growth
5	1092	86.0	241	2 JI0097	nerve growth facto
6	1073	84.5	303	1 NGRTBA	nerve growth facto
7	788.5	62.1	243	2 A26311	nerve growth facto
8	773	60.9	235	2 S14481	nerve growth facto
9	675.5	53.2	243	2 A51193	nerve growth facto
10	658	51.8	155	2 A26312	nerve growth facto
11	649	51.1	246	2 A59218	nerve growth facto
12	484	38.1	117	2 S28161	nerve growth facto
13	481.5	37.9	124	2 IS1709	nerve growth facto
14	481.5	37.9	257	2 C40304	nerve growth facto
15	472	37.2	258	2 S09155	neurotrophin-3 pre
16	471.5	37.1	257	2 IS0400	neurotrophin-3 pre
17	471	37.1	282	2 A35781	hippocampus-derive
18	452.5	35.6	116	1 NGNMXI	nerve growth facto
19	448.5	35.3	116	2 A58566	nerve growth facto
20	436	33.5	286	2 S50855	nerve growth facto
21	365	28.7	247	2 A40304	neurotrophin-6 - s
22	364	28.7	249	2 B40304	brain-derived neur
23	360	28.3	249	2 S12555	brain-derived neur
24	358.5	28.2	252	2 A30361	brain-derived neur
25	348.5	27.4	248	2 JC6183	brain-derived neur
26	343	27.0	226	2 JH0400	neurotrophin-4 pre
27	337.5	26.6	210	2 A42687	neurotrophin-4 pre
28	335	26.4	269	2 IS1708	brain-derived neur
29	330.5	26.0	209	2 B42687	neurotrophin-4 pre

30	323.5	25.5	114	2	184765	brain-derived neur
31	316.5	24.9	114	2	150606	brain-derived neur
32	307.5	24.2	114	2	151599	brain-derived neur
33	84.5	6.7	5126	2	840450	ryanodine receptor
34	83	6.5	397	2	S53782	aspartic proteinas
35	80	6.3	835	2	C97322	probable alpha-ara
36	79.5	6.3	749	2	E86774	hypothetical prote
37	79	6.2	807	2	A53225	ecdysone-induced p
38	78.5	6.2	1095	2	T24061	hypothetical prote
39	78.5	6.2	513	2	A12555	hypothetical prote
40	78.5	6.2	701	2	T52384	hypothetical prote
41	78.5	6.2	742	2	T43520	condensin complex
42	78.5	6.2	1076	2	D82083	carbamoyl-phosphat
43	78.5	6.2	1084	2	B64088	hemoglobin-binding
44	78.5	6.2	1609	2	B87243	probable cation tr
45	78	6.1	323	2	S69647	hypothetical prote

ALIGNMENTS

RESULT 1

NGHUM
nerve growth factor beta chain precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999
C/Accession: A01399; S10253
R/Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.
Nature 303, 821-825, 1983
A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mouse
A/Reference number: A93305; MUID:83244969; PMID:6688123
A/Accession: A01399
A/Molecule type: DNA
A/Residues: 1-286 <URL>
R/Borsani, G.; Pizzuti, A.; Ruggeri, E.I.; Pallini, A.; Silani, V.; Sidoli, A.; Scarlato
Nucleic Acids Res. 18, 4020, 1990
A/Title: cDNA sequence of human beta-NGF.
A/Reference number: S10253; MUID:90326556; PMID:2374737
A/Accession: S10253
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 46-286 <BOR>
A/Cross-references: EMBL:X52599; NID:929476; PIDD:CA36832.1; PID:G29477
C/Comment: Nerve growth factor is found in submaxillary gland in large quantities and in
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels ma
C/Genetics:
A/Gene: GDB:NGFB
A/Cross-references: GDB:120233; OMIM:162030
A/Map position: 1p13.1-1p13.1
A/Intons: 41/3
C/Superfamily: nerve growth factor is composed of two alpha chains, two beta chains, and tw
C/Keywords: glycoprotein; growth factor; submandibular gland
F:1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>
F:167-284/Product: nerve growth factor beta chain #status predicted <MAT>
F:267,114,159,211/Binding site: carbonylate (asn) (covalent) #status predicted
F:181-246,224-274,234-276/disulfide bonds: #status predicted

Query Match 100.0%; Score 1270; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILIGIOAEPHSNSNPAGHTTPOVWMTLQHSLDPLRALRARAAPAAIA 60
DB 46 MSMLFYTLITAFILIGIOAEPHSNSNPAGHTTPOVWMTLQHSLDPLRALRARAAPAAIA 105
QY 61 ARVAGQTRNITVDPRFLFKRRRLSPVLFSTQPPREAADTODLDFVGAAPNRTTRSK 120
DB 106 ARVAGQTRNITVDPRFLFKRRRLSPVLFSTQPPREAADTODLDFVGAAPNRTTRSK 165
QY 121 RSSSHPIFRGERSVCDSDSVWVGDKTTATYDITKGEVMTLGEVINNSVFKOYFFETKCR 180
DB 166 RSSSHPIFRGERSVCDSDSVWVGDKTTATYDITKGEVMTLGEVINNSVFKOYFFETKCR 225

QY 181 DPNVDSGCRGIDSKHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 240
Db 226 DPNVDSGCRGIDSKHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 285
QY 241 A 241
Db 286 A 286

RESULT 2

146614
nerve growth factor B - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C/Accession: 146614
R/LabId: Mamsais, Y., Mellink, C., Yerde, M., Gellin, J.
Cytogenet. Cell Genet. 67, 120-125, 1994
A/Title: A new marker (NGFB) on pig chromosome 4, isolated by using consensus sequence
A/Reference number: 146614; MUID:94313891; PMID:8039422
A/Accession: 146614
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-229 <L&H>
A/Cross-references: GB:IJ3898; NID:9476732; PIDN:AAA21301.1; PID:9533771
A/Genetics:
A/Gene: NGFB
C/Superfamily: nerve growth factor beta chain

Query Match 88.54; Score 1124; DB 2; Length 229;
Best Local Similarity 92.64; Pred. No. 2.7e-99;
Matches 212; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 13 LIGIOAPHSNSVNPAGHTIPVHMTLQHSIDTALRRASAPAAIAAVAGOTNITV 72
Db 1 LIGIOAPHSNSVNPAGHTIPVHMTLQHSIDTALRRASAPAAIAAVAGOTNITV 60
QY 73 DPLFLFKRRRLRSRVLFSSTPPREADTODLDEVGGAAPFNTTHSKSSHPFIRHGE 132
Db 61 DPLFLFKRRRLRSRVLFSSTPPREADTODLDEVGGAAPFNTTHSKSSHPFIRHGE 120
QY 133 FSVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETKCRDNPVDSGCRGI 192
Db 121 FSVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETKCRDNPVDSGCRGI 180
QY 193 DSGHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 241
Db 181 DSGHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 229

RESULT 3

156570
beta-nerve growth factor - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C/Accession: 156570
R/LabId: Mamsais, Y., Mellink, C., Yerde, M., Gellin, J.
Cytogenet. Cell Genet. 67, 120-125, 1994
A/Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippocampus
A/Reference number: 156570; MUID:89037223; PMID:3184206
A/Accession: 156570
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-245 <RES>
A/Cross-references: GB:M36589; NID:9205691; PIDN:AAA1697.1; PID:9205692
C/Superfamily: nerve growth factor beta chain

Query Match 87.24; Score 1107; DB 2; Length 245;
Best Local Similarity 85.84; Pred. No. 1.2e-96;
Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSMLFTLTALFAGIOAPHSNSVNPAGHTIPVHMTLQHSIDTALRRASAPAAIA 60
Db 1 MSMLFTLTALFAGIOAPHSNSVNPAGHTIPVHMTLQHSIDTALRRASAPAAIA 60

Db 5 MSMLFTLTALFAGIOAPHSNSVNPAGHTIPVHMTLQHSIDTALRRASAPAAIA 64
QY 61 ARVAGOTNITVDPRLFKRRRLRSRVLFSSTPPREADTODLDEVGGAAPFNTTHSK 120
Db 65 ARVAGOTNITVDPRLFKRRRLRSRVLFSSTPPREADTODLDEVGGAAPFNTTHSK 124
QY 121 RSSHPIFRHGEVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETKCR 180
Db 125 RSSHPIFRHGEVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETKCR 184
QY 181 DPNVDSGCRGIDSKHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 240
Db 185 DPNVDSGCRGIDSKHNSVCTTHTFPVKALTMGKQAMRFIRIDTACVLSRKAVR 244

RESULT 4

NGMSMG
nerve growth factor beta chain precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Nov-1980 #sequence_revision 19-Feb-1984 #text_change 21-Jul-2000
C/Accession: A93301; A93305; A90366; I49689; I52891; A01400; I49690
R/Scott, J., Selby, M., Urdet, M., Quiroga, M., Bell, G.T., Rutter, W.J.
Nature 302, 538-540, 1983
A/Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse nerve growth factor
A/Reference number: A93301; MUID:83167518; PMID:6336309
A/Accession: A93301
A/Molecule type: mRNA
A/Residues: 1-307 <SCO>
A/Cross-references: GB:V00836; NID:953364; PIDN:CAA24221.1; PID:953365
R/Ollrich, A., Gray, A., Berman, C., Dull, T.J.
Nature 303, 821-825, 1983
A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mouse nerve growth factor
A/Reference number: A93305; MUID:83244969; PMID:6688123
A/Accession: A93305
A/Molecule type: mRNA
A/Residues: 1-307 <L&H>

A/Cross-references: GB:K01759; NID:920051; PIDN:AAA9820.1; PID:9387495
A/Note: these authors believe that Met-67 is probably the amino-terminal residue and t
R/Angelini, R.H., Herndon, M.A., Bradshaw, R.A.
Biochemistry 12, 100-115, 1973
A/Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and cha
A/Reference number: A90366; MUID:73075048; PMID:4566923
A/Accession: A90366
A/Molecule type: protein
A/Residues: 188-216; N, 218-305 <ANG>
R/Selby, M.J., Edwards, R., Sharp, F., Rutter, W.J.
Mol. Cell. Biol. 7, 3057-3064, 1987
A/Title: Mouse nerve growth factor gene: Structure and expression.
A/Reference number: I49689; MUID:88038855; PMID:3670305
A/Accession: I49689
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-307 <RES>
A/Cross-references: GB:M17298; NID:9193493; PIDN:AAA7667.1; PID:9467311
R/Ollrich, A., Gray, A., Berman, C.H., Coussens, L., Dull, T.J.
Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983
A/Title: Sequence homology of human and mouse beta-NGF subunit genes.
A/Reference number: I52891; MUID:84206565; PMID:6327169
A/Accession: I52891
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-307 <RES>
A/Cross-references: GB:M14805; NID:9200053; PIDN:AAA39821.1; PID:9200054
C/Comment: The active molecule is a dimer of identical chains associated by noncovalen
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels in
C/Genetics:
A/Gene: NGFB
A/Introns: 21/2, 62/3
C/Superfamily: nerve growth factor beta chain
C/Keywords: glycoprotein; growth factor; homodimer
F.1-187/Domain: signal sequence and propeptide #status predicted <Sig>
F.188-305/Product: nerve growth factor beta chain #status experimental <Mat>

F135,180/Binding site: carbohydrate (asn) (covalent) #status predicted
F1202,267,245,255,297/Diulfide bonds: #status experimental
F1232/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 86.3%; Score 1096; DB 1; Length 307;
Best Local Similarity 85.0%; Pred. No. 1,76-95;
Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
DB 67 MSMLFYTLITAFILGIGQAEPTDSNVPSBDSVPEAHWTLOHSIDTALRRASAPAAIA 126
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
DB 127 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 186
QY 121 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 180
DB 187 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 246
QY 181 DPNPVDSCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 240
DB 247 ASNPFVSGCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 306

RESULT 5

JL0097
nerve growth factor beta chain precursor - guinea pig

C/Species: Cavia porcellus (guinea pig)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Mar-1996
C/Accession: JL0097

R/Schwartz, M.A.; Fisher, D.; Bradshaw, R.A.; Isaacson, P.J.
J. Neurochem. 52, 1203-1209, 1989

A/Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig
A/Reference number: JL0097; MUID:89177243; PMID:2926397
A/Accession: JL0097
A/Molecule type: mRNA
A/Residues: 1-241 <SC>
A/Note: the authors translated the codon GCU for residue 214 as Asp

C/Genetics:
A/Gene: Beta-NGF
C/Superfamily: nerve growth factor beta chain
C/Keywords: glycoprotein; growth factor; hormone
F1-121/Domain: propeptide #status predicted <PRO>
F122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F146-154/Region: receptor binding #status predicted
F169,114/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 86.0%; Score 1092; DB 2; Length 241;
Best Local Similarity 86.2%; Pred. No. 2,9e-95;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
QY 121 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 180
DB 121 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDSCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 240

RESULT 6

NGRTBA
nerve growth factor beta chain precursor - multimammate rat (Mastomys natalensis)
C/Species: Mastomys natalensis

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C/Accession: J0343
R/Fahnestock, M.; Bell, R.A.
Gene 69, 257-264, 1988

A/Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from Mastomys natalensis
A/Reference number: J0343; MUID:89172070; PMID:3234767
A/Accession: J0343
A/Molecule type: mRNA
A/Residues: 1-303 <FA>
A/Cross-references: GB:M22748; NID:G202514; PIDN:AAA40599.1; PID:G202515
A/Note: It is uncertain whether Met-1 or Met-63 is the initiator

C/Superfamily: nerve growth factor beta chain
C/Keywords: glycoprotein; growth factor; homodimer; submaxillary gland
F184-301/Product: nerve growth factor beta chain #status predicted <MAT>
F131,176,228/Binding site: carbohydrate (asn) (covalent) #status predicted
F198-263,241-291,251-293/Diulfide bonds: #status predicted

Query Match 84.5%; Score 1073; DB 1; Length 303;
Best Local Similarity 83.3%; Pred. No. 2,4e-93;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
DB 63 MSMLFYTLITAFILGIGQAEPTDSNVPSBDSVPEAHWTLOHSIDTALRRASAPAAIA 122
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
DB 123 ARVAGQTRNITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 182
QY 121 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 180
DB 183 RSSHPHFHGEFSCVSVWVGDKTTATDICKKEMVTLGEVINNSVFKQYFEETKCR 242
QY 181 DPNPVDSCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 240
DB 243 ASNPFVSGCRGIDSKHNSYCTTHTFVKALTMGKOAAFRIRIDTACVLSKRAVR 302

RESULT 7

A26311
nerve growth factor beta chain precursor - chicken (fragment)

C/Species: Gallus gallus (chicken)
C/Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000
C/Accession: A26311; A24857; S00127; S12532
R/Ebendal, T.; Larhammar, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986

A/Title: Structure and expression of the chicken beta nerve growth factor gene.
A/Reference number: A26311; MUID:86300646; PMID:3017695
A/Accession: A26311
A/Molecule type: mRNA
A/Residues: 1-243 <EB>

A/Cross-references: GB:X04003; NID:G63697; PIDN:CAA27633.1; PID:G1334740
FEB5 Lett. 203, 82-86, 1986
A/Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in chicken embryo
A/Reference number: A24857; MUID:86248129; PMID:3720959
A/Accession: A24857
A/Molecule type: DNA
A/Residues: 118-243 <MO>

A/Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:G222840; PIDN:BA00008.1; PID:R10000
R/Mon, D.; Perret, C.; Frechlin, N.; Keller, A.; Behar, G.; Brachet, P.; Aufferay, C.
EMBO J. 5, 1489-1493, 1986
A/Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in chicken embryo

A/Reference number: A26312; MUID:86300647; PMID:2427334
A/Accession: S00127
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 121-243 <ME>

A/Cross-references: GB:M26810; NID:G212446; PIDN:AAA48984.1; PID:G212447
R/Ibanez, C.F.; Haliboseck, F.; Ebendal, T.; Persson, H.
EMBO J. 9, 1477-1483, 1990
A/Title: Structure-function studies of nerve growth factor: functional importance of his-100
A/Reference number: S12532; MUID:90228346; PMID:2328722

A/Accession: S12532
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 126-243 <1BA>
C/Superfamily: nerve growth factor beta chain
C/Keywords: growth factor
F/1-125/Domain: signal sequence #status predicted <SIG>
F/126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match 62.1%; Score 788.5; DB 2; Length 243;
Best Local Similarity 64.9%; Pred. No. 1,1e-66;
Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSNPAAG---HTIPQVMTKLOHSLDTALRRASAPA 56
DB 5 MSMLYTLITLTAFLIGIOAEPHSSNPAAG---HTIPQVMTKLOHSLDTALRRASAPA 57
QY 57 AAIARVA-----GOTRNTITVDPLPKRRLRSRVLFTSTOPPREADTODLDFEVGAAPN 111
DB 58 TT-HGRFAMPDGTEDLNINADQNFKKRRFRSSVLFSTOPPREADTODLDFEVGAAPN 115
QY 112 PENTHRKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 171
DB 116 SLNRTARTKR-TAHPVLRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 174
QY 172 QYFETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVC 231
DB 175 QYFETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVC 234
QY 232 VLSRKAVR 239
DB 235 VLSRKSGR 242

RESULT 8

S14481
nerve growth factor beta chain precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C/Accession: S14481
R/Carrier: F.; Campbell, M.; Cardinale, B.; Pierandrei-Amaldi, P.
submitted to the EMBL Data Library, October 1990
A/Description: Structure and expression of the nerve growth gene in Xenopus oocyte and
A/Reference number: S14481
A/Accession: S14481
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-235 <CAR>
A/Cross-references: EMBL:X55716; NID:g64914; PIRN:CAA39249.1; PID:g64915
C/Superfamily: nerve growth factor beta chain

Query Match 60.9%; Score 773; DB 2; Length 235;
Best Local Similarity 63.6%; Pred. No. 3,2e-65;
Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSNPAAG---HTIPQVMTKLOHSLDTALRRASAPA 54
DB 5 MSMLYTLITLTAFLISVQAAPEKTDHAPRSASAKSRIPHHTRTKSLHNS-----53
QY 55 PAALIAARVAGQTNITVDPLPKRRLRSRVLFTSTOPPREADTODLDFEVGAAPN 114
DB 54 -HGKLEAKERSYFRNVTVDPLPKRRLRSRVLFTSTOPPREADTODLDFEVGAAPN 111
QY 115 RTHRSKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 174
DB 112 KTRARAR-TAHPVLRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 170
QY 175 PENTHRKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 234
DB 171 PENTHRKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 230
QY 235 RK 236

DB 231 RK 232

RESULT 9

151193
nerve growth factor precursor - many-banded krait
C/Species: Bungarus multicinctus (many-banded krait)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C/Accession: 151193
R/Danese, J.M.; Garnier, J.M.
Growth Factors 8, 77-86, 1993
A/Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from th
A/Accession: 151193
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-243 <DAN>
A/Cross-references: GB:S56212; NID:g266298; PIRN:AA825729.1; PID:g266299
C/Superfamily: nerve growth factor beta chain

Query Match 53.2%; Score 675.5; DB 2; Length 243;
Best Local Similarity 56.8%; Pred. No. 5e-56;
Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSNPAAG---HTIPQVMTKLOHSLDTALRRASAPA 56
DB 1 MSMLYTLITLTAFLIGIWAAPKSDNVLGSPAKSDFSDTCAQTHGLKTSRNTDQHPT 60
QY 57 AAIARVA-----GOTRNTITVDPLPKRRLRSRVLFTSTOPPREADTODLDFEVGAAPN 115
DB 61 PKSEDOELGSANNTIYDPLPKRRLRSRVLFTSTOPPREADTODLDFEVGAAPN 119
QY 116 THRSKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 175
DB 120 NINA-NENHPVANGSHSVCDISVWVNTKRTATIKGNTVWVDVNNENVYKQYFF 178
QY 176 ETRCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVC 235
DB 179 ETRCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVC 238
QY 236 K 236
DB 239 K 239

RESULT 10

A26312
nerve growth factor beta chain precursor - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
C/Accession: A26312
R/Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A/Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
A/Reference number: A26312; MUID:86300647; PMID:2427334
A/Accession: A26312
A/Molecule type: mRNA
A/Residues: 1-125 <MEI>
A/Cross-references: GB:M26809; NID:g163419; PIRN:AAA3066.1; PID:g163420
C/Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embry
C/Superfamily: nerve growth factor beta chain
C/Keywords: growth factor; homodimer; seminal vesicle
F/6-125/Product: nerve growth factor #status predicted <MAT>
F/20-85,63-113,73-115/Diulfide bonds: #status predicted

Query Match 51.8%; Score 658; DB 2; Length 125;
Best Local Similarity 95.2%; Pred. No. 9,8e-55;
Matches 119; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 117 HRSKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 176
DB 1 HRSKSSSHPIFRGGEFVSVDVSVWVGDKTATDICKKEVWVLGEVNNINSVFK 176

QY 177 TKCRDPNVDGSGCGIDSKHNSYCTTTHFEVKALTMGKQAAFRIRIDPACVLSRK 236
 DB 61 TKCRDPNVDGSGCGIDSKHNSYCTTTHFEVKALTMGKQAAFRIRIDPACVLSRK 120
 QY 237 AVRA 241
 DB 121 TGORA 125

RESULT 11

AS9218

nerve growth factor beta chain precursor - mononocled cobra
 C/Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 C/Accession: A59218; S13965
 R/Selby, M.J.; Edwards, R.H.; Rutter, W.J.
 J. Neurosci. Res. 18, 293-298, 1987
 A/Title: Cobra nerve growth factor: structure and evolutionary comparison.
 A/Reference number: A59218; PMID:88090976; PMID:3694772
 A/Accession: A59218

A/Molecule type: mRNA
 A/Residues: 1-246 <SEL>
 R/Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayaishi, K.
 FEBS Lett. 279, 38-40, 1991
 A/Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
 A/Reference number: S13927; PMID:9118785; PMID:1995338
 A/Accession: S13965
 A/Molecule type: protein
 A/Residues: 131-246 <IND>
 A/Experimental source: Venom
 C/Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
 C/Complex: homodimer
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: growth factor; homodimer; venom
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/131-246/Product: nerve growth factor beta chain #status experimental <MAT>
 F/144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match 51.1%; Score 649; DB 2; Length 246;
 Best Local Similarity 55.6%; Pred. No. 1.6e-53;
 Matches 134; Conservative 30; Mismatches 69; Indels 8; Gaps 5;

QY 1 NMMLPTTLTALFLIGQABPHSSNPAG---HTTPQVHTLQHSIDTLRRASAP 56
 DB 6 NMMLCTTILAFILIGWAAPKSEDNVPLSPATSDLSCTHGLKTSRNTDQHPA 65
 QY 57 AAIARVAGOT-RNTVDPRLFKQRLRSRVLFSFOPPREADTDODLPEVGGAPPR 115
 DB 66 POKAEDDELRTANITVDPLFKQKROSPRVLFSFOPPLSRDESVF-LDNEDSLNR 124
 QY 116 THRSKRSSHPFHRGEFSCDSVSVWVDKTTATDIDKGEVWVLGEVINNSVFKQYFF 175
 DB 125 NIFAR-R-EDHPVHNGEHSVCDVSAMV-TKTTAIDIKENTYVMEANVLNDRVYQYFF 182
 QY 176 EFKCDPNVDGSGCGIDSKHNSYCTTTHFEVKALTMGKQAAFRIRIDPACVLSRK 235
 DB 183 EFKCNPDPPEGSGCGIDSHNSYCTETDTFIALTMGNOQASWRFIRIETACVLRK 242
 QY 236 K 236
 DB 243 K 243

RESULT 12

S28161

nerve growth factor beta chain - Russell's viper
 C/Species: Viper russelli (Russell's viper)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C/Accession: S28161
 R/Koyama, Y.; Inoue, S.; Ikeda, K.; Hayaishi, K.
 Biochim. Biophys. Acta 1160, 287-292, 1992
 A/Title: Purification and amino-acid sequence of a nerve growth factor from the venom of
 A/Reference number: S28161; PMID:93120151; PMID:1477101

A/Accession: S28161
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-117 <KOY>
 C/Superfamily: nerve growth factor beta chain

Query Match 38.1%; Score 484; DB 2; Length 117;
 Best Local Similarity 74.1%; Pred. No. 2.2e-38;
 Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

RESULT 13

151709

nerve growth factor beta chain precursor - southern platyfish
 C/Species: Xiphophorus maculatus (southern platyfish)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C/Accession: 151709; S26674
 R/Gotz, R.; Raulf, F.; Scharf, M.
 J. Neurochem. 59, 432-442, 1992
 A/Title: Brain-derived neurotrophic factor is more highly conserved in structure and f
 A/Reference number: 151708; PMID:92333301; PMID:1629719
 A/Accession: 151709
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-194 <GOT>
 A/Cross-references: EMBL:X59941; NID:g65277; PID:CAA42566.1; PID:g65278
 C/Genetics:
 A/Gene: NGF
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein; growth factor
 F/1-14/Domain: signal sequence #status predicted <SIG>
 F/15-79/Domain: propeptide #status predicted <PRO>
 F/80-194/Product: nerve growth factor beta chain #status predicted <MAT>
 F/90-155,133-183,143-185/Disulfide bonds: #status predicted
 F/99/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.9%; Score 481.5; DB 2; Length 194;
 Best Local Similarity 58.9%; Pred. No. 7.1e-38;
 Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

QY 71 TVDPRLFKKRLRSRVLFSFOPPREADTDODLPE-VGGAAPFNRTRSKRSSHPFH 129
 DB 40 TVDPRLFKKRLRSRVLFSFOPPREADTDODLPE-VGGAAPFNRTRSKRSSHPFH 83
 QY 130 RGEFSCDSVSVWVDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCDPNVDGSGC 189
 DB 84 RGEVSCDSVSVWVDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCDPNVDGSGC 143
 QY 190 RGDIDSKHNSYCTTTHFEVKALTMGKQAAFRIRIDPACVLSRK 237
 DB 144 LGIDARHNSHCTNSHTFVRLTSSSENVAMRLIRINAVCAVCVLSRK 191

RESULT 14

C40304

neurotrophin-3 precursor - human
 N/Alternate names: nerve growth factor 2; NGF-2
 C/Species: Homo sapiens (man)
 C/Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C/Accession: A36208; JH0141; C40304; S107129; C60536
 R/Jones, K.R.; Reichardt, L.F.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990
 A/Title: Molecular cloning of a human gene that is a member of the nerve growth factor
 A/Reference number: A36208; PMID:91045937; PMID:2236018
 A/Accession: A36208

A/Molecule type: DNA
 A/Residues: 1-257 <JON>
 A/Cross-references: GB:M37763; NID:g189300; PIDN:AAA5953.1; PID:g189301
 R/Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nikolic
 Neuron 4, 767-773, 1990
 A/Title: Primary structure and biological activity of a novel human neurotrophic factor
 A/Reference number: JH0141; MUID:90262727; PMID:2344409
 A/Accession: JH0141
 A/Molecule type: DNA
 A/Residues: 1-257 <ROS>
 R/Maisompierre, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la M
 Genomics 10, 558-568, 1991
 A/Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struc
 A/Reference number: A40304; MUID:91365361; PMID:1869806
 A/Accession: C40304
 A/Molecule type: DNA
 A/Residues: 1-257 <NAI>
 A/Cross-references: GB:M61180; NID:g189302; PIDN:AAA63231.1; PID:g189303
 R/Kaiho, Y.; Yoshimura, K.; Nakahama, K.
 FEBS Lett. 266, 187-191, 1990
 A/Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.
 A/Reference number: S10719; MUID:90306351; PMID:2365067
 A/Accession: S10719
 A/Molecule type: mRNA
 A/Residues: 1-257 <KAI>
 A/Cross-references: GB:X53555; NID:g287794; PIDN:CAA37703.1; PID:g287795
 R/Yancopoulos, G.D.; Maisompierre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
 A/Title: Neurotrophic factors, their receptors, and the signal transduction pathways the
 A/Reference number: A60536; MUID:9211157; PMID:1966766
 A/Accession: C60536
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-73, 'Q', 75-77, 'R', 79-108, 'T', 110-257 <YAN>
 C/Genetics:
 A/Genes: GDB:NTP3
 A/Cross-references: GDB:125917; OMIM:162660
 A/Map position: 12p13-12p13
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/139-138/Domain: propeptide #status predicted <PRO>
 F/139-257/Product: neurotrophin-3 #status predicted <MAT>
 F/131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.9%; Score 481.5; DB 2; Length 257;
 Best Local Similarity 40.7%; Pred. No. 1e-37;
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;

QY 1 MSMLFYTLITAFILGIGQAPHSSENVPAHTIPQV-----HWTXLQHSID 45
 DB 1 MSILFYVFLAYLRIQGNNDQSLPEDSLNSLIKLIQADILKNKLSKQWVDKENYQ 60
 QY 46 TALARRA-----RSAPAAALAAVAGOTRNTITVDPRLFK-RRRLSRPVLFSTOPPREA 97
 DB 61 STLPRKAEPREPREGGPAKSAFOV-----TAMDTELRQQRYSNPRVLLSDSTPLEP 114
 QY 98 ADTQDLDFEVGAAPFNRTHSRKSSHPHFRRGFSVCDSSVWVGDTTATDIDGKEV 157
 DB 115 PELYLMEDYVGSPPVANNRTSRKRYAEHK-SHGRGYSVCDSESLWTDKSSALIDRGHQV 173
 QY 158 MWLGEVNNINSVFKYFEETKCRDNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GK 216
 DB 174 TVLGSIKTGNSEPVKQFYETCKEARPVKNGCRGIDDKHNSOCTISQTYRALTSENNK 233
 QY 217 QAAMFRIDTACVCLSRKAVR 239
 DB 234 LVGRMRIRIDTSVCALSRKIGR 256

RESULT 15
 S09155
 neurotrophin-3 precursor - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #ext_change 16-Jul-1999
 C/Accession: S09155; S51179
 R/Rohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.
 Nature 344, 339-341, 1990
 A/Title: Identification and characterization of a novel member of the nerve growth fa
 A/Reference number: S09155; MUID:90190865; PMID:2314473
 A/Accession: S09155
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-258 <HON>
 A/Cross-references: GB:X53257; NID:g53451; PIDN:CAA37348.1; PID:g53452
 R/Kolbeck, R.; Jungbluth, S.; Barde, Y.A.
 Eur. J. Biochem. 225, 995-1003, 1994
 A/Title: Characterisation of neurotrophin dimers and monomers.
 A/Reference number: S51179; MUID:95045576; PMID:7957235
 A/Accession: S51179
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 140-152 <ROL>
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/140-258/Product: neurotrophin-3 #status predicted <MAT>
 F/131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.2%; Score 472; DB 2; Length 258;
 Best Local Similarity 41.9%; Pred. No. 8e-37;
 Matches 108; Conservative 33; Mismatches 97; Indels 20; Gaps 5;

QY 1 MSMLFYTLITAFILGIGQAPHSSENVPAH-----TIPQVHTXLQHSIDTL----- 48
 DB 1 MSILFYVFLAYLRIQGNNDQSLPEDSLNSLIKLIQADILKNKLSKQWVDKENYQ 60
 QY 49 -----RRRSAPAAALAAVAGOTRNTITVDPRLFKRRRLSRPVLFSTOPPREADTQDL 103
 DB 61 STLPRKAEPREPREGGPAKSAFOV-----TAMDTELRQQRYSNPRVLLSDSTPLEPPLYM 120
 QY 104 DFEVGAAPFNRTH-RSKRSSHPHFRRGFSVCDSSVWVGDTTATDIDGKEVMTGE 162
 DB 121 EDYGNPVPANNRTSPRKRKYAEHK-SHGRGYSVCDSESLWTDKSSALIDRGHQVTVLGE 179
 QY 163 VNINNSVFKYFEETKCRDNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GKQAAVR 221
 DB 180 IKTGNSEPVKQFYETCKEARPVKNGCRGIDDKHNSOCTISQTYRALTSENNKLVGR 239
 QY 222 FIRIDTACVCLSRKAVR 239
 DB 240 WIRIDTSVCALSRKIGR 257

Search completed: June 6, 2003, 10:51:33
 Job time: 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:49:38 ; Search time 17.5 Seconds
(without alignments)
1421.766 Million cell updates/sec

Title: US-09-788-188-1

Perfect score: 1270

Sequence: 1 MSMFTTITAFLLIGIQAEPP.....FIRIDTACVTSRRKAVRRA 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1270	100.0	241	8	US-08-450-842-5
2	1270	100.0	241	9	US-09-788-188-1
3	1270	100.0	241	9	US-10-150-262-3
4	1270	100.0	241	9	US-10-155-886-1
5	1270	100.0	241	9	US-10-155-886-6
6	1270	100.0	242	12	US-10-072-681-1
7	1265	99.7	241	10	US-09-822-263-16
8	1265	99.6	241	9	US-09-788-188-2
9	1249	98.3	241	9	US-10-155-886-7
10	1107	87.2	241	9	US-10-155-886-8
11	1106	87.1	231	9	US-10-155-886-10
12	1095	86.3	241	9	US-10-155-886-9
13	788.5	62.1	243	9	US-10-155-886-11
14	773	60.9	235	9	US-10-155-886-12
15	651	51.3	120	9	US-10-150-262-1
16	648	51.0	120	9	US-10-155-886-34
17	648	51.0	121	12	US-10-072-681-2
18	648	51.0	157	10	US-09-798-338-4
19	647.5	51.0	167	10	US-09-798-338-8

20	642	50.6	153	10	US-09-798-338-2	Sequence 2, Appl1
21	642	50.6	163	10	US-09-798-338-6	Sequence 6, Appl1
22	621	48.9	121	9	US-09-813-398-9	Sequence 9, Appl1
23	619	48.7	121	9	US-10-155-886-33	Sequence 33, Appl1
24	602	47.4	120	9	US-10-155-886-36	Sequence 36, Appl1
25	584	46.0	118	9	US-10-155-886-40	Sequence 40, Appl1
26	584	46.0	120	9	US-10-155-886-38	Sequence 38, Appl1
27	584	46.0	121	12	US-10-072-681-3	Sequence 3, Appl1
28	566	44.6	117	9	US-10-155-886-42	Sequence 42, Appl1
29	512	40.3	121	9	US-10-155-886-37	Sequence 37, Appl1
30	505	39.8	125	9	US-10-155-886-35	Sequence 35, Appl1
31	481.5	37.9	257	8	US-08-450-842-4	Sequence 4, Appl1
32	481.5	37.9	257	9	US-09-788-188-5	Sequence 5, Appl1
33	481.5	37.9	257	9	US-10-155-886-3	Sequence 3, Appl1
34	476.5	37.5	257	9	US-09-788-188-6	Sequence 6, Appl1
35	474	37.3	260	9	US-10-155-886-20	Sequence 20, Appl1
36	472	37.2	258	9	US-10-155-886-18	Sequence 18, Appl1
37	471.5	37.1	257	9	US-10-155-886-19	Sequence 19, Appl1
38	471	37.1	258	9	US-10-155-886-17	Sequence 17, Appl1
39	452	35.6	142	8	US-08-450-842-52	Sequence 52, Appl1
40	390	30.7	72	10	US-09-848-664-21	Sequence 21, Appl1
41	388.5	30.6	119	10	US-09-745-032-6	Sequence 6, Appl1
42	388.5	30.6	119	10	US-09-742-600-6	Sequence 6, Appl1
43	388.5	30.6	119	10	US-09-872-090-6	Sequence 3, Appl1
44	388.5	30.6	120	10	US-09-745-032-3	Sequence 3, Appl1
45	388.5	30.6	120	10	US-09-742-600-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-08-450-842-5

Sequence 5, Application US/08450842

Patent No. US20020045576A1

GENERAL INFORMATION:

APPLICANT: GENE TECH, INC.

APPLICANT: ROSENTHAL, ARNON

TITLE OR INVENTION: NOVEL NEUROTROPIC FACTOR

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450, 842

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy B.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 666P2C1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-450-842-5

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 241 A 241
 241 A 241

RESULT 2
 US-09-788-188-1
 Sequence 1, Application US/09788188
 Publication No. US20030040082A1

GENERAL INFORMATION:
 APPLICANT: TUSZYSKI, MARK
 APPLICANT: BLESCH, ARMIN
 TITLE OF INVENTION: MUTANT PRO-NEUTROPHIN WITH IMPROVED ACTIVITY
 FILE REFERENCE: 041673/2045
 CURRENT APPLICATION NUMBER: US/09/788,188
 CURRENT FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-788-188-1

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240

Qy 241 A 241
 Db 241 A 241

RESULT 3
 US-10-150-262-3
 Sequence 3, Application US/10150262
 Publication No. US20030049264A1
 GENERAL INFORMATION:
 APPLICANT: FOSTER, KEITH ALAN
 APPLICANT: DUGGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
 TITLE OF INVENTION: PERIPHERAL SENSORY APPARENT FUNCTIONS
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/10/150,262
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US/09/447,356
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-10-150-262-3

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 1 MSMLFTLTITAFILGIGQAEPSHESNPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTRSK 120
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVNNINSVFQYFFETKCR 180
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 241 A 241
 241 A 241

RESULT 4
 US-10-155-886-1
 Sequence 1, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Kenneth K.
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pounel
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1, 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-1

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 180
 QY 181 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 240
 DB 181 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

US-10-155-886-6
 Sequence 6, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:

APPLICANT: Hemstead, Barbara L.
 APPLICANT: Lee, Kamee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pounesh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 6
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-6

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 180
 QY 181 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 240
 DB 181 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 240

QY 241 A 241
 DB 241 A 241

RESULT 6

US-10-072-681-1
 Sequence 1, Application US/10072681
 Patent No. US20020137893A1
 GENERAL INFORMATION:

APPLICANT: Burton, Louis R.
 APPLICANT: Schmelzer, Charles H.
 APPLICANT: Beck, Joanne T.
 TITLE OF INVENTION: PURIFICATION OF NGF
 FILE REFERENCE: GENENT 037C3
 CURRENT APPLICATION NUMBER: US/10/072, 681
 CURRENT FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: 60/030838
 PRIOR FILING DATE: 1996-11-15
 PRIOR APPLICATION NUMBER: 60/047855
 PRIOR FILING DATE: 1997-05-29
 PRIOR APPLICATION NUMBER: 08/970865
 PRIOR FILING DATE: 1997-11-14
 PRIOR APPLICATION NUMBER: 09/363573
 PRIOR FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/675,503
 PRIOR FILING DATE: 2000-09-29
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-072-681-1

Query Match 100.0%; Score 1270; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 2 MSMLFTLLTAFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 61
 QY 61 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 62 ARVAGGTNTITVDPRLFKKRLRSFVLFSTQPPREAADTODLDFEVGAAPFNRTRSK 121
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 180
 DB 122 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVININNSVFKQYFEETKCR 181
 QY 181 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 240
 DB 182 DPNPVDSCGCGIDSKHMNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRKAVER 241
 QY 241 A 241
 DB 242 A 242

RESULT 7

US-09-822-263-16
 Sequence 16, Application US/09822263
 Patent No. US20020036598A1
 GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas
 APPLICANT: Vernet, Corine
 APPLICANT: Shinkete, Richard A
 APPLICANT: Burgess, Catherine
 APPLICANT: Spytek, Kimberly
 APPLICANT: Tchernyev, Velizar T
 TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded T
 FILE REFERENCE: 15966-572 C1P1

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/ CURRENT APPLICATION NUMBER: US/09/822,263
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 09/672,665
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/156,745
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 60/158,942
/ PRIOR FILING DATE: 1999-10-06
/ PRIOR APPLICATION NUMBER: 60/159,248
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: 60/169,344
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 60/215,048
/ PRIOR FILING DATE: 2000-06-23
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-822-263-16

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Query Match          99.7%; Score 1266; DB 10; Length 241;
Best Local Similarity 99.6%; Pred. No. 6e-124;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 8
US-09-788-188-2
/ Sequence 2, Application US/09788188
/ Publication No. US20030040082A1
/ GENERAL INFORMATION:
/ APPLICANT: TUSZYNSKI, MARK
/ APPLICANT: BLESCH, ARMTN
/ TITLE OF INVENTION: MUTANT PRO-NEUROTROPHIN WITH IMPROVED ACTIVITY
/ FILE REFERENCE: 041673/2045
/ CURRENT APPLICATION NUMBER: US/09/788,188
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Mutant NGF
/ OTHER INFORMATION: pro-neurotrophin
US-09-788-188-2

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Query Match          99.6%; Score 1265; DB 9; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.6e-124;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 9
US-10-155-886-7
/ Sequence 7, Application US/10155886
/ Publication No. US20030087804A1
/ GENERAL INFORMATION:
/ APPLICANT: Hempstead, Barbara L.
/ APPLICANT: Lee, Ramona K.
/ APPLICANT: Teng, Kenneth K.
/ TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
/ FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
/ CURRENT APPLICATION NUMBER: US/10/155,886
/ CURRENT FILING DATE: 2002-08-05
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patent In version 3.1
/ SEQ ID NO 7
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Gorilla gorilla
US-10-155-886-7

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Query Match          98.3%; Score 1249; DB 9; Length 241;
Best Local Similarity 98.8%; Pred. No. 3.6e-122;
Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTYLTAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

```

```

RESULT 10
US-10-155-886-8
/ Sequence 8, Application US/10155886
/ Publication No. US20030087804A1
/ GENERAL INFORMATION:
/ APPLICANT: Hempstead, Barbara L.

```

APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 8
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-155-886-8

Query Match 87.2%; Score 1107; DB 9; Length 241;
 Best Local Similarity 85.8%; Pred. No. 2.3e-107;
 Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

1 MSMLPYTLITAFILGIAQEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 1 MSMLPYTLITAFILGIAQEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 61 ARVAGQTNITVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 61 ARVAGQTNITVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 121 RSSHPPIFRHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 121 RSSHPPIFRHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 121 RSTHPVFMHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 161 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240
 161 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240
 181 ASNPVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240

RESULT 11
 US-10-155-886-10
 Sequence 10, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 10
 LENGTH: 231
 TYPE: PRT
 ORGANISM: Bos taurus
 US-10-155-886-10

Query Match 87.1%; Score 1106; DB 9; Length 231;
 Best Local Similarity 90.7%; Pred. No. 2.7e-107;
 Matches 205; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

11 AFLIGIOAEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIAARVAGQTNIT 70
 1 AFLIGIOAEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIAARVAGQTNIT 70
 71 TVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSSSHPIFHR 130
 71 TVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSSSHPIFHR 130
 61 TVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSSSHPIFHR 120
 61 TVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSSSHPIFHR 120
 131 GEPVDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCRDPNVDGCR 190
 131 GEPVDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCRDPNVDGCR 190
 121 GEPVDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCRDPNVDGCR 180

QY 191 GIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSK 236
 DB 181 GIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSK 226

RESULT 12
 US-10-155-886-9
 Sequence 9, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 9
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-155-886-9

Query Match 86.3%; Score 1096; DB 9; Length 241;
 Best Local Similarity 85.0%; Pred. No. 3.2e-106;
 Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

1 MSMLPYTLITAFILGIAQEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 1 MSMLPYTLITAFILGIAQEPHSESNVPAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 61 ARVAGQTNITVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 61 ARVAGQTNITVDPRLFKKRLSPRLVFTSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 121 RSSHPPIFRHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 121 RSSHPPIFRHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 121 RSTHPVFMHGEFVSVCDSVWVGDKTTATDICKKEVWVLGEVINNSVFQYFETKCR 180
 161 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240
 161 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240
 181 ASNPVDSGCRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSKAVRR 240

RESULT 13
 US-10-155-886-11
 Sequence 11, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 11
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Gallus gallus
 US-10-155-886-11

Query Match 62.1%; Score 788.5; DB 9; Length 243;
 Best Local Similarity 64.9%; Pred. No. 3.7e-74;
 Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;
 1 MSMLPYTLITAFILGIAQEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 56

```

Db 5 MSMLYTLITLITLITGQAAPKSEDNQPLEVPAHSHSPSTQOSGCHT-----ATAAQ 57
Qy 57 AATAAFAVA-----GQRTNITVDRLFKRRLSPVLFSTOPPREADTODLDFEVGA 111
Db 58 TT-HGFAPWMPDGTEDLNTAMDQNFKKRFRSSRLVFGTQPPVSRKQOSTGF-LSAV 115
Qy 112 PPRTRRSKSSSHPIFHNGEFSVCDSVSWVGDKTATDIDKGEVVLGEVNNINSVK 171
Db 116 SLNRTRATYR-TNHPVLHNGEFSVCDSVSWVGDKTATDIDKGEVTVLGEVNNINSVK 174
Qy 172 QYFETKCRDPNPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVC 231
Db 175 QYFETKCRDPNPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVC 234
Qy 232 VLSRKA VR 239
Db 235 VLSRKSGR 242

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```

RESULT 14
US-10-155-886-12
; Sequence 12, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hemstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kernani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-155-886-12

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Query Match 60.9%; Score 773; DB 9; Length 235;
Best Local Similarity 63.6%; Pred. No. 1.5e-72;
Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;
Qy 1 MSMLYTLITLITLITGQAAPKSEDNQPLEVPAHSHSPSTQOSGCHT-----ATAAQ 57
Db 5 MSMLYTLITLITLITGQAAPKSEDNQPLEVPAHSHSPSTQOSGCHT-----ATAAQ 57
Qy 55 PAAAIARVAGQCTNITVDRLFKRRLSPVLFSTOPPREADTODLDFEVGAAPFN 114
Db 54 -HGTLBAKEPSYFNVTVDPLFRKRFRSPVLFSTQPPPLSDFQHLEY-LDDESLN 111
Qy 115 RTHSRKSSSHPIFHNGEFSVCDSVSWVGDKTATDIDKGEVVLGEVNNINSVK 171
Db 112 KTIRAKR-TNHPVLHNGEFSVCDSVSWVGDKTATDIDKGEVTVLGEVNNINSVK 170
Qy 175 FETKCRDPNPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVC 234
Db 171 FETKCRDPNPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVC 230
Qy 235 RK 236
Db 231 RK 232

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RESULT 15
US-10-150-262-1
; Sequence 1, Application US/10150262
; Publication No. US20030049264A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, KEITH ALAN
; APPLICANT: DUGGAN, MICHAEL JOHN

```

```

; APPLICANT: SHONE, CLIFFORD CHARLES
; TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
; TITLE OF INVENTION: PERIPHERAL
; FILE REFERENCE: 023223/0104
; CURRENT FILING DATE: 2002-05-20
; PRIOR FILING DATE: 1998-01-12
; PRIOR FILING DATE: 1999-11-22
; PRIOR FILING DATE: 1998-01-12
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-150-262-1

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Query Match 51.3%; Score 651; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 122 SSSHPIFRGEFSVCDSVSWVGDKTATDIDKGEVVLGEVNNINSVKQYFETKCRD 181
Db 1 SSSHPIFRGEFSVCDSVSWVGDKTATDIDKGEVVLGEVNNINSVKQYFETKCRD 60
Qy 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVCVLSRKA VR 241
Db 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDPACVCVLSRKA VR 120

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Search completed: June 6, 2003, 10:52:46
 Job time: 18.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:48:22 ; Search time 12.5 Seconds
(without alignments)
567.274 Million cell updates/sec

Title: US-09-788-188-1

Perfect score: 1270
Sequence: 1 MSHLFTYLRFLIGIQAE.....FIRIDTACVLSRRKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patente AA.*
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2: /cgn2_6/ptodate/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodate/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodate/1/1aa/6B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1270	100.0	241	1	US-08-266-080B-4
2	1270	100.0	241	1	US-08-451-947-5
3	1270	100.0	241	2	US-08-424-826A-5
4	1270	100.0	241	2	US-08-595-043A-75
5	1270	100.0	241	3	US-08-970-865-1
6	1270	100.0	241	3	US-08-928-694-5
7	1270	100.0	241	4	US-09-363-573-1
8	1270	100.0	241	4	US-09-447-356-3
9	1270	100.0	241	5	PCT-US91-06950-5
10	1270	100.0	241	5	PCT-US95-05423-4
11	1270	100.0	242	4	US-09-675-503-1
12	996	78.4	240	3	US-08-910-691-11
13	651	51.3	120	1	US-08-440-049-3
14	651	51.3	120	2	US-08-441-513A-3
15	651	51.3	120	3	US-08-581-662-31
16	651	51.3	120	4	US-08-845-541B-1
17	651	51.3	120	4	US-09-066-065A-1
18	651	51.3	120	4	US-09-447-356-1
19	651	51.3	120	5	US-09-664-295-31
20	651	51.3	120	5	PCT-US95-06918-3
21	648	51.0	120	3	US-08-970-865-2
22	648	51.0	120	4	US-09-363-573-2
23	648	51.0	121	4	US-09-675-503-2
24	648	51.0	157	4	US-09-675-922-4
25	647.5	51.0	167	4	US-09-675-922-8
26	642	50.6	119	3	US-08-753-642-2
27	642	50.6	153	4	US-09-675-922-2

28	642	50.6	163	4	US-09-675-922-6	Sequence 6, Appl1
29	637	50.2	120	4	US-08-845-541B-3	Sequence 3, Appl1
30	637	50.2	120	4	US-09-066-065A-3	Sequence 3, Appl1
31	634	49.9	120	4	US-08-845-541B-4	Sequence 4, Appl1
32	634	49.9	120	4	US-09-066-065A-4	Sequence 4, Appl1
33	629	49.5	120	4	US-08-845-541B-12	Sequence 12, Appl1
34	629	49.5	120	4	US-09-066-065A-12	Sequence 12, Appl1
35	628	49.4	120	4	US-08-845-541B-17	Sequence 17, Appl1
36	628	49.4	120	4	US-08-845-541B-20	Sequence 20, Appl1
37	628	49.4	120	4	US-09-066-065A-17	Sequence 17, Appl1
38	628	49.4	120	4	US-09-066-065A-20	Sequence 20, Appl1
39	626	49.3	120	4	US-08-845-541B-21	Sequence 21, Appl1
40	626	49.3	120	4	US-09-066-065A-18	Sequence 18, Appl1
41	626	49.3	120	4	US-09-066-065A-21	Sequence 21, Appl1
42	626	49.3	120	4	US-08-845-541B-13	Sequence 13, Appl1
43	623	49.1	120	4	US-08-845-541B-19	Sequence 19, Appl1
44	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl1
45	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
APPLICATION DATA:
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
US-08-266-0808-4

Query Match 100.0%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAMRFRIIDTACVLSRAVRR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAMRFRIIDTACVLSRAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 2
US-08-451-947-5
Sequence 5, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENE TECH, INC.
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2CID2
TELEPHONE: 415/952-8674
TELEFAX: 415/952-8681
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-5

Query Match 100.0%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAMRFRIIDTACVLSRAVRR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAMRFRIIDTACVLSRAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 3
US-08-424-826A-5
Sequence 5, Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,826A
FILING DATE: 19-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P066P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-424-826A-5

Query Match 100.0%; Score 1270; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIQAEPSHSNVPAGHTTPOVHTWLQHSLDLALRRASAPAAATA 60
DB 1 MSMLFTLLTAFLIGIQAEPSHSNVPAGHTTPOVHTWLQHSLDLALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTSRK 120
DB 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTSRK 120
QY 121 RSSSHPIFRGSPVCDVSVMVGDKTTATDIKGEVWLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSPVCDVSVMVGDKTTATDIKGEVWLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-08-595-043A-75
Sequence 75, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-595-043A-75

Query Match 100.0%; Score 1270; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIQAEPSHSNVPAGHTTPOVHTWLQHSLDLALRRASAPAAATA 60
DB 1 MSMLFTLLTAFLIGIQAEPSHSNVPAGHTTPOVHTWLQHSLDLALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTSRK 120
DB 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTSRK 120
QY 121 RSSSHPIFRGSPVCDVSVMVGDKTTATDIKGEVWLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGSPVCDVSVMVGDKTTATDIKGEVWLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 5

US-08-970-865-1
Sequence 1, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-6005081-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-970-865-1

Query Match 100.0%; Score 1270; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILIGIAEPHSESNVPAAGHTIPQVHTKLOHSLDTLRRARSAPAAIA 60
DB 1 MSMLFYTLITAFILIGIAEPHSESNVPAAGHTIPQVHTKLOHSLDTLRRARSAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKRRRLSPRLVFTSTOPPREADTODLDFEVGGAAPFRTRRSK 120
DB 61 ARVAGOTRNTITVDPRLFKRRRLSPRLVFTSTOPPREADTODLDFEVGGAAPFRTRRSK 120
QY 121 RSSSHPIFRHGEFVSCDSVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFVSCDSVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241

RESULT 6

US-08-928-694-5
Sequence 5, Application US/08928694
Patent No. 6037320

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-Sep-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-928-694-5

Query Match 100.0%; Score 1270; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILIGIAEPHSESNVPAAGHTIPQVHTKLOHSLDTLRRARSAPAAIA 60
DB 1 MSMLFYTLITAFILIGIAEPHSESNVPAAGHTIPQVHTKLOHSLDTLRRARSAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKRRRLSPRLVFTSTOPPREADTODLDFEVGGAAPFRTRRSK 120
DB 61 ARVAGOTRNTITVDPRLFKRRRLSPRLVFTSTOPPREADTODLDFEVGGAAPFRTRRSK 120
QY 121 RSSSHPIFRHGEFVSCDSVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFVSCDSVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241

RESULT 7

US-09-363-573-1
Sequence 1, Application US/09363573
Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis B. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-363-573-1

Query Match 100.0%; Score 1270; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 QY 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLFSTQPPREADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLFSTQPPREADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 8
 US-09-447-356-3
 Sequence 3, Application US/09447356
 Patent No. 6395513
 GENERAL INFORMATION:
 APPLICANT: FOSTER, KEITH ALAN
 APPLICANT: DUGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/09/447,356
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-09-447-356-3

Query Match 100.0%; Score 1270; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 QY 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLFSTQPPREADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLFSTQPPREADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240

DB 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9
 PCT-US91-06950-5

Sequence 5, Application PC/TUS9106950
 GENERAL INFORMATION:
 APPLICANT: GENENTECH, INC.
 APPLICANT: ROSENTHAL, ARNON
 TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06950
 FILING DATE: 19910924
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/646482
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hensley, Max D.
 REGISTRATION NUMBER: 27,043
 REFERENCE/DOCKET NUMBER: 666P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1994
 TELEFAX: 415/952-9881
 TELE: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-06950-5

Query Match 100.0%; Score 1270; DB 5; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
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 DB 61 ARVAGQTRNITVDPRLFKKRRRLSPRVLFSTQPPREADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIGIDSKMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10
PCT-US95-05423-4
Sequence 4, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: STNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
PCT-US95-05423-4
Query Match 100.0%; Score 1270; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTRLRARSAPAAIA 60
Db 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTRLRARSAPAAIA 60

Qy 61 ARVAGQTNITVDPLFKKRLRSPRLVSTQPPREADTDODLDFEVGGAAPFNTRHSK 120
Db 61 ARVAGQTNITVDPLFKKRLRSPRLVSTQPPREADTDODLDFEVGGAAPFNTRHSK 120
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Db 121 RSSSHPIFRGSEFVSCDSVSWVGDKTATIKGKENVVLGEVNNINSVPKQYFEETCR 180
Qy 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSKAVAR 240
Db 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSKAVAR 240
Qy 241 A 241
Db 241 A 241
RESULT 11
US-09-675-503-1
Sequence 1, Application US/09675503
Patent No. 6423831
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
FILE REFERENCE: GENENT. 03702
CURRENT APPLICATION NUMBER: US/09/675,503
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-675-503-1
Query Match 100.0%; Score 1270; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTRLRARSAPAAIA 60
Db 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTRLRARSAPAAIA 61
Qy 61 ARVAGQTNITVDPLFKKRLRSPRLVSTQPPREADTDODLDFEVGGAAPFNTRHSK 120
Db 62 ARVAGQTNITVDPLFKKRLRSPRLVSTQPPREADTDODLDFEVGGAAPFNTRHSK 121
Qy 121 RSSSHPIFRGSEFVSCDSVSWVGDKTATIKGKENVVLGEVNNINSVPKQYFEETCR 180
Db 122 RSSSHPIFRGSEFVSCDSVSWVGDKTATIKGKENVVLGEVNNINSVPKQYFEETCR 181
Qy 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSKAVAR 240
Db 182 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMQKQAMRFIRIDTACVCLSKAVAR 241
Qy 241 A 241
Db 242 A 242
RESULT 12

US-08-910-691-11
Sequence 11, Application US/08910691
Patent No. 6015552
GENERAL INFORMATION:
APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/074,969
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-691-11

Query Match 78.4%; Score 996; DB 3; Length 240;
Best Local Similarity 79.2%; Pred. No. 3.9e-110;
Matches 190; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

DB 1 MSMLFYLLITFLIGIQAEPSHSNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
1 MSMLFYLLITFLIGIQAEPSHSNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60

QY 61 ARVAGOTRNTIVDRLPFKRLRSRPRVCFSTOPREADTODLDPREVGGAAPFRTHRSK 120
61 ARVAGOTRNTIVDRLPFKRLRSRPRVCFSTOPREADTODLDPREVGGAAPFRTHRSK 120

DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCR 180
121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCR 180

QY 121 RYAEHR-SHNGEYVCCSSELMVTDKSSALIDIRHQVYVLEIKTNGSPVQYFETKCR 179
121 RYAEHR-SHNGEYVCCSSELMVTDKSSALIDIRHQVYVLEIKTNGSPVQYFETKCR 179

DB 181 DPNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVR 239
181 DPNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVR 239

QY 180 EARPVXKGCIGIDDKHNSQCKTSQTYVRAITSENNKLVGRWIRIDTSCVCAISRKIGR 239
180 EARPVXKGCIGIDDKHNSQCKTSQTYVRAITSENNKLVGRWIRIDTSCVCAISRKIGR 239

RESULT 13
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.

APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANROPIC NEUTROTROPIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino acid
TOPOLOGY: linear
US-08-440-049-3

Query Match 51.3%; Score 651; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCRD 181
122 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCRD 181

DB 1 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCRD 60
1 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFQYFETKCRD 60

QY 182 PNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVRA 241
182 PNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVRA 241

DB 61 PNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVRA 120
61 PNPVDGCGGIDSKKMSYCTTHTTTPYKALTMG-KQAAMRFIRIDTACVLSRKAVRA 120

RESULT 14
US-08-441-513A-3
Sequence 3, Application US/08441513A
Patent No. 5981480
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Panotropic Neurotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-441-513A-3

Query Match	51.3%	Score 651;	DB 2;	Length 120;
Best Local Similarity	100.0%	Pred. No. 1.3e-69;		
Matches 120; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

RESULT 15
US-08-581

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: Sequence 31, Application US/08581662
: Patent No. 6121235
: GENERAL INFORMATION:
: APPLICANT: Gao, Mei-Qiang
: TITLE OF INVENTION: Treatment of Balance Impairments
: FILE REFERENCE: P0981
: CURRENT APPLICATION NUMBER: US/08/581,662
: CURRENT FILING DATE: 1995-12-29
: NUMBER OF SEQ ID NOS: 36
: SEQ ID NO 31
: LENGTH: 120
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-08-581-662-31

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Query Match	51.3%	Score 651	DB 3	Length 120
Best Local Similarity	100.0%	Pred. No. 1.3e-69		
Matches 120; Conservative	0	Mismatches	0	Gaps 0

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Job time : 13.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:46:22 ; Search time 32.5 Seconds

(without alignments)
988.105 Million cell updates/sec

Title: US-09-788-188-1

Sequence: 1 MSMLFYTLITAFILIGIOAF.....FIRIDTACVCLSKRAVRA 241

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
4	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
5	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
6	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
7	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
8	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
9	1270	100.0	241	12	AA13063 Human NGF Smal-Apa
10	1270	100.0	241	12	AA13063 Human NGF Smal-Apa

11	1270	100.0	241	23	AB04994
12	1270	100.0	245	5	AA040038
13	1267	99.8	307	14	AA15241
14	1266	99.7	241	22	AA067865
15	1266	99.7	307	14	AA137799
16	1264	99.5	307	19	AA069725
17	1238	97.5	239	14	AA13910
18	1188.5	93.6	241	12	AA13886
19	1175	92.5	222	21	AA090884
20	1096	86.3	240	23	AA050845
21	1096	86.3	307	5	AA040036
22	1093	86.3	307	14	AA040038
23	1093	86.1	307	14	AA040038
24	996	78.4	240	14	AA043937
25	996	78.4	240	13	AA056451
26	991	78.0	240	13	AA056451
27	682	53.7	129	14	AA037539
28	682	53.7	129	14	AA037539
29	661	52.0	124	13	AA024145
30	657.5	51.8	124	13	AA021851
31	651	51.3	120	20	AA022751
32	651	51.3	120	21	AA029141
33	651	51.3	120	22	AA044994
34	651	51.3	120	22	AA035944
35	648	51.0	156	23	AA050303
36	648	51.0	157	21	AA001596
37	648	51.0	157	22	AA067677
38	648	51.0	157	23	AA085725
39	647.5	51.0	166	23	AA050301
40	647.5	51.0	167	22	AA067679
41	647	50.9	261	10	AA091299
42	647	50.9	262	7	AA061033
43	643	50.6	120	17	AA090531
44	642	50.6	118	10	AA091034
45	642	50.6	119	5	AA000040

ALIGNMENTS

RESULT 1	AA13063	AA13063 standard; Protein; 241 AA.
AC	AA13063;	
DT	30-SEP-1991 (first entry)	
DE	Human NGF Smal-Apai fragment prod.	
KW	Expression vector; human nerve growth factor; yeast;	
KM	senile dementia.	
XX		
OS	Homo sapiens.	
XX		
PN	JP03139285-A.	
XX		
PD	13-JUN-1991.	
XX		
PF	20-DEC-1989; 89UP-0328199.	
XX		
PR	27-JUL-1989; 89UP-0192581.	
XX		
PA	(TAKE) TAKEDA CHEMICAL IND KK.	
XX		
DR	WPI; 1991-218449/30.	
XX		
DR	N-PSDB; AAQ12638.	
XX		
PT	New yeast expression vector - used in produ. of human nerve growth	
XX	factor from corresp. yeast.	
XX		
PS	Disclosure; Fig 1(1-2); 14pp; Japanese.	
XX		

Human beta nerve g
Sequence encoded b
Human pre-pro nerv
Amino acid sequenc
Human NGF. Homo 8
Human beta-nerve g
Nerve growth facto
NGF with pro-regio
Human proNGF prote
Mouse nerve growth
Sequence encoded b
Cloned mouse pre-p
Sequence of pro re
NGF/NT-3 in PTB13
Recombinant beta-N
Chimeric neurotrop
Human growth facto
N-terminal of neut
Nerve growth facto
NGF-beta amino aci
Nerve growth facto
Nerve growth facto
Amino acid sequenc
Synthetic nerve gr
Nerve growth facto
Amino acid sequenc
Human nerve growth
Human beta-nerve g
Panlropic neurotro
Human nerve growth
Sequence encoded b

WPI; 1991-059398/09.

PA (TAKE) TAKEDA CHEMICAL, IND KK.

PA (TAKE) TAKEDA CHEMICAL IND KK.

DR WPI; 1991-269694/37.
 DR N-PSDB; AAQ13397.
 XX Secretory prep. of animal protein - by culturing
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of
 PT promoter region.
 XX
 PS Disclosure; Fig 3; 12pp; Japanese.
 CC The amino acid sequence is encoded that of human nerve growth factor
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the
 CC glyceraldehyde-3-phosphate dehydrogenase (GAD) gene promoter.
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 12; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQNTITVDPRLFKKRLRSFRLFSTOPPREAADTODLDFEVGGAAPFRTRSK 120
 DB 61 ARVAGQNTITVDPRLFKKRLRSFRLFSTOPPREAADTODLDFEVGGAAPFRTRSK 120
 QY 121 RSSSHPIFHRGSEFSCDSVSWVGDKTTATDIDKGEVMTLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFHRGSEFSCDSVSWVGDKTTATDIDKGEVMTLGEVINNSVFKQYFETKCR 180
 QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 4
 AAR77419
 ID AAR77419 standard; Protein; 241 AA.
 AC AAR77419;
 DT 10-FEB-1996 (first entry)
 DE Human nerve growth factor.
 KW Nerve growth factor; neurotrophic factor; therapeutic;
 KW protein refolding; NGF.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Protein 122..241
 FT /note= "mature protein"
 FT Region 1..121
 FT /note= "pre-region"
 XX
 PN MO9530686-A1.
 PD 16-NOV-1995.
 PF 02-MAY-1995; 95NC-US05423.
 PR 27-JUN-1994; 94US-0266080.
 PR 09-MAY-1994; 94US-0240122.
 PA (SYNT) SYNTAX-SYNERGEN NEUROSCIENCE JOINT VENTU.
 XX Bonam D, Kohno T, Lile J, Rosendahl MS;

XX WPI; 1995-404080/51.
 DR N-PSDB; AAT05437.
 XX Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.
 XX
 PS Disclosure; Page 33-34; 57pp; English.
 CC The nerve growth factor (NGF) gene is expressed in Escherichia
 CC coli cells. The recombinant protein is solubilized and
 CC sulfonlated and allowed to refold in the presence of ppg and urea.
 CC Biologically active NGF, used for promoting the survival of and
 CC maintaining the phenotypic differentiation of nerve and glial cells,
 CC is isolated and purified. This method breaks incorrectly formed
 CC disulphide bonds and allows refolding of the factor into the correct
 CC tertiary structure required for maximum yield of full active protein.
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 16; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQNTITVDPRLFKKRLRSFRLFSTOPPREAADTODLDFEVGGAAPFRTRSK 120
 DB 61 ARVAGQNTITVDPRLFKKRLRSFRLFSTOPPREAADTODLDFEVGGAAPFRTRSK 120
 QY 121 RSSSHPIFHRGSEFSCDSVSWVGDKTTATDIDKGEVMTLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFHRGSEFSCDSVSWVGDKTTATDIDKGEVMTLGEVINNSVFKQYFETKCR 180
 QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 5
 AAR66688
 ID AAR66688 standard; Protein; 241 AA.
 AC AAR66688;
 DT 23-AUG-1995 (first entry)
 DE Human nerve growth factor.
 KW Human nerve growth factor; hNGF; polyclonal antibody;
 KW immunogen; enzyme immunoassay.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= sig_peptide
 FT Peptide 19..121
 FT /label= pro_peptide
 FT /note= "corresponding codon TCG"
 FT /note= "corresponding codon TAT"
 FT /note= "corresponding codon TAG"
 FT /note= "corresponding codon TAG"
 FT Disulfide-bond 136..201

FH Key Location/Qualifiers
 FT Protein 1..121
 FT /label= Prepro_region
 FT Protein 122..241
 FT /label= Mat_protein
 FT Modified-site 167
 FT /note= "N-glycosylated"
 FT Region 179..189
 FT /note= "conserved Cys-containing region involved in
 FT Cys knot motif"
 FT Region 229..231
 FT /note= "conserved Cys-containing region involved in
 FT Cys knot motif"
 FT Region 241..241
 FT /note= "conserved Cys-containing region involved in
 FT Cys knot motif"
 XX MO9821234-A2.
 XX 22-MAY-1998.
 XX 14-NOV-1997; 97MO-US21068.
 XX 29-MAY-1997; 97US-0047855.
 XX 15-NOV-1996; 96US-0030838.
 PA (GERTH) GENENTECH INC.
 PT Beck JT, Burton LE, Schmelzer CH;
 PT WPI; 1998-322333/28.
 XX
 XX Isolation of neurotrophin(s) from, e.g. mls-folded or glycosylated
 PT variant(s) - using hydrophobic interaction chromatography,
 PT optionally in combination with high performance cation exchange
 PT chromatography
 XX
 PS Disclosure; Fig 4; 59pp; English.
 CC This polypeptide comprises the human nerve growth factor (NGF)
 CC beta chain precursor. Methods are provided for large-scale
 CC purification of neurotrophins, including mature NGF, suitable for
 CC clinical use. A claimed method comprises: (1) separating the
 CC neurotrophin from the other proteins using a hydrophobic
 CC interaction chromatography resin (HICR); and optionally (2)
 CC separating the neurotrophin from a chemical variant by high
 CC performance cation exchange chromatography (HPEC). The processes
 CC can also be used for purification of e.g. mouse NGF (see AAM48887),
 CC brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5
 CC (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow
 CC separation of neurotrophins from various undesirable misprocessed,
 CC misfolded, size, glycosylated or charge forms. They allow selective
 CC separation from their variants and other molecules, and from other
 CC polypeptides with high pI. The processes are applicable to
 CC starting materials from various sources, including fermentation
 CC broths or lysed bacterial or mammalian cells.
 CC
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 19; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRARAPAAIA 60
 DB 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRARAPAAIA 60
 QY 61 ARVAGOTRNTTVPRLFKKRLRSPRLSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGOTRNTTVPRLFKKRLRSPRLSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 QY 122 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 122 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDGCGRIGDSKMNYSCTTHTFVKALTMGQAMRFIRIDPACVLSRKAVER 240
 DB 181 DPNPVDGCGRIGDSKMNYSCTTHTFVKALTMGQAMRFIRIDPACVLSRKAVER 240

DB 181 DPNPVDGCGRIGDSKMNYSCTTHTFVKALTMGQAMRFIRIDPACVLSRKAVER 240
 QY 241 A 241
 DB 241 A 241
 RESULT 8
 ID AAY07303
 ID AAY07303 standard; Protein; 241 AA.
 XX AAY07303;
 XX 06-JUL-1999 (first entry)
 XX
 XX Human nerve growth factor beta protein.
 XX Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF2;
 KW expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;
 KW NT3; voluntary motor function.
 XX
 OS Homo sapiens.
 XX
 XX MO9900148-A2.
 XX 07-JAN-1999.
 XX 30-JUN-1998; 98MO-US13778.
 XX 30-JUN-1997; 97US-0051255.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PT Gage FH, Grill R, Tuszynski MH;
 PT WPI; 1999-095478/08.
 DR N-PSDB; AAX34366.
 XX
 XX Treating spinal cord injuries in a mammal - by inducing growth of
 PT cerebrospinal projection axons using a recombinant vector for
 PT expressing CST neurotrophin
 XX
 PS Disclosure; Fig 6; 49pp; English.
 CC The invention relates to a method of inducing cerebrospinal projection
 CC (CST) axon growth in a mammal with a spinal cord injury that involves
 CC a CST lesion by delivering a recombinant expression vector for CST
 CC neurotrophin, such as this sequence - nerve growth factor beta. The
 CC method is used to induce partial recovery of voluntary motor function.
 CC in a mammal after disruption of corticospinal projections in the spinal
 CC cord.
 CC
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 20; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRARAPAAIA 60
 DB 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRARAPAAIA 60
 QY 61 ARVAGOTRNTTVPRLFKKRLRSPRLSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGOTRNTTVPRLFKKRLRSPRLSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDKGEVMVLGEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDGCGRIGDSKMNYSCTTHTFVKALTMGQAMRFIRIDPACVLSRKAVER 240
 DB 181 DPNPVDGCGRIGDSKMNYSCTTHTFVKALTMGQAMRFIRIDPACVLSRKAVER 240

Db 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 Db 241 A 241

RESULT 9
 AAB66929
 ID AAB66929 standard; Protein; 241 AA.

AC AAB66929;
 DT 17-APR-2001 (first entry)
 XX
 XX Human NGF.
 DE Human.
 XX Human; neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KM Huntington's chorea; nerve damage; nerve growth factor; NGF.
 XX Homo sapiens.
 OS US6174701-B1.
 FN 16-JAN-2001.
 PD 31-MAY-1995; 95US-0455741.
 XX 15-MAR-1990; 90US-0494024.
 PR 31-JAN-1995; 95US-0381030.
 PR 12-DEC-1989; 89US-0449811.
 XX (GERTH) GENENTECH INC.
 PA Rosenthal A, Winslow JW;
 FI WPI; 2001-201803/20.
 DR
 XX New nucleic acid encoding a neuronal factor (rat precursor
 PT neurotrophin-3; NT-3), useful in the recombinant preparation of NT-3,
 PT which is useful for enhancing the survival of nerve cells and treating
 PT neurodegenerative diseases -
 XX
 PS Disclosure; Fig 3; 18pp; English.

CC The present invention relates to neuronal factor (NF) also known as
 CC neurotrophin-3/NT-3; see AAF55829-AAF5830 and AAB66927-AAB66928). NF
 CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's chorea and other conditions
 CC characterised by necrosis or loss of neurons. NF is also useful for
 CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such
 CC as burns or wounds. The present sequence is human nerve growth factor
 CC (NGF), which was used in a sequence homology alignment with human NF
 CC protein.
 XX
 XX Sequence 241 AA;
 SQ

Query Match 100.0%; Score 1270; DB 22; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLLTAPLIGIOAEPSHSNVPAGHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 Db 1 MSMLFYLLTAPLIGIOAEPSHSNVPAGHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 QY 61 ARVAGGTNITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 Db 61 ARVAGGTNITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFHHGSEVCDVSVWGDKTATDIDKGEVNLGEVNNINSVEKQYFFETKCR 180
 Db 121 RSSSHPIFHHGSEVCDVSVWGDKTATDIDKGEVNLGEVNNINSVEKQYFFETKCR 180
 QY 121 RSSSHPIFHHGSEVCDVSVWGDKTATDIDKGEVNLGEVNNINSVEKQYFFETKCR 180
 Db 121 RSSSHPIFHHGSEVCDVSVWGDKTATDIDKGEVNLGEVNNINSVEKQYFFETKCR 180

QY 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVR 240
 Db 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 Db 241 A 241

RESULT 10
 AAE18904
 ID AAE18904 standard; Protein; 241 AA.

AC AAE18904;
 DT 21-MAY-2002 (first entry)
 XX
 XX Human beta nerve growth factor (NGF) protein.
 DE Human.
 XX Human; nerve growth factor; NGF; neurotrophin; cholinergic neuron;
 KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;
 KM neurodegenerative condition; ALS; amyotrophic lateral sclerosis.
 XX Homo sapiens.
 OS W0200207774-A2.
 FN 31-JAN-2002.
 PD 17-MAY-2001; 2001WO-US16122.
 PF 19-JUL-2000; 2000US-0620174.
 PR (REGC) UNIV CALIFORNIA.
 PA Tuszynski MH;
 FI WPI; 2002-195846/25.
 DR N-PSDB; AAD30144.
 DR
 XX Delivering therapeutic neurotrophin to targeted defective, diseased or
 PT damaged cholinergic neurons, useful for treating neurodegenerative
 PT disease, comprises administering a neurotrophin encoding transgene into
 PT the brain -
 XX
 PS Example 1; Fig 2; 38pp; English.

CC The invention relates to a method for delivering therapeutic neurotrophin
 CC to targeted defective, diseased or damaged cholinergic neurons in
 CC the mammalian brain. The method comprises delivering a neurotrophic
 CC composition comprising a neurotrophin encoding transgene into one or more
 CC delivery sites within a region of the brain containing targeted neurons.
 CC The method is useful for treating neurodegenerative conditions such as
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis
 CC (ALS) in primates by stimulating the growth of neurons thus recovering
 CC neurological function. The present sequence is human nerve growth factor
 CC (NGF-2) protein which is a neurotrophin.
 XX
 XX Sequence 241 AA;
 SQ

Query Match 100.0%; Score 1270; DB 23; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLLTAPLIGIOAEPSHSNVPAGHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 Db 1 MSMLFYLLTAPLIGIOAEPSHSNVPAGHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 QY 61 ARVAGGTNITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 Db 61 ARVAGGTNITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120

QY 121 RSSHPHFHGRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSHPHFHGRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGCGIDSKHMNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDSCGCGIDSKHMNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 11
 ID ABB04994 standard; Protein; 241 AA.
 AC ABB04994;
 DE 19-MAR-2002 (first entry)
 XX Human beta nerve growth factor protein.
 XX
 XX Human: nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;
 KW neurotrophin-3; nervous system growth factor; neuronal atrophy;
 KW aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;
 KW anti-aging; cholinergic neuron growth stimulator; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX US2001043920-A1.
 PD 22-NOV-2001.
 PF 05-DEC-2000; 2000US-0730790.
 XX
 XX 15-APR-1998; 98US-0060543.
 PA (TUSZ/) TUSZYNSKI M H.
 PA (BLES/) BLESCH A.
 XX
 PI Tuszynski MH, Blesch A;
 DR WPI; 2002-105567/14.
 DR N-PSDB; ABA92503.
 XX
 PT Ameliorating neuronal atrophy and loss of accompanying normal aging
 PT comprises delivering a transgene encoding a growth factor to a
 PT mammalian brain to stimulate axon growth in cholinergic neurons -
 PS Disclosure; Fig 6 1-2; 18pp; English.
 XX
 XX The present invention describes a method for ameliorating neuronal
 CC atrophy and loss of accompanying normal aging in the mammalian brain.
 CC The method comprises delivering a growth factor (GF)-encoding transgene
 CC to preselected delivery sites in the brain, so that the encoded GF is
 CC expressed in the brain and stimulates axonal growth in targeted
 CC GF-receptive neurons. The growth factor has neurotrophic, neuroprotective
 CC and anti-aging activities, and can be used as a cholinergic neuron
 CC growth stimulator and in gene therapy. The method is used to
 CC ameliorating neuronal atrophy and loss of accompanying normal aging, in
 CC the human brain. The present sequence represents human beta nerve growth
 CC factor, which is given in the exemplification of the present invention.
 XX
 SO Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 23; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSNLFYTLITAFILGIGQAEPHSSENVPAGHTIPQVMTKLOHSLDTALRRARSAAPAAIA 60
 DB 1 MSNLFYTLITAFILGIGQAEPHSSENVPAGHTIPQVMTKLOHSLDTALRRARSAAPAAIA 60

QY 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREADTODLDFEVGGAAPFNTRRSK 120
 DB 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREADTODLDFEVGGAAPFNTRRSK 120
 QY 121 RSSHPHFHGRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSHPHFHGRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 QY 241 A 241
 DB 241 A 241
 RESULT 12
 ID AAP40038 standard; Protein; 245 AA.
 AC AAP40038;
 DE 25-JAN-1992 (first entry)
 XX Sequence encoded by portion of human beta-nerve growth factor
 DE (NGF) chromosomal gene which includes an exon.
 XX
 XX Nerve damage; therapy.
 XX
 XX Homo sapiens.
 XX
 XX EP121338-A.
 PD 10-OCT-1984.
 PF 02-MAR-1984; 84EP-0301377.
 XX
 XX 03-MAR-1983; 83US-0471962.
 PA (GETH) GENENTECH INC.
 XX
 PI Gray AM, Ullrich A;
 DR WPI; 1984-251909/41.
 DR N-PSDB; AAN40033.
 XX
 PT Human beta-nerve growth factor free from other proteins - obtd.
 PT by recombinant DNA techniques for treating nerve damage
 PS Example; Fig 5; 42pp; English.
 XX
 XX The inventors claim human beta-nerve growth factor (NGF) free from
 CC other proteins of human origin. Also claimed are the DNA sequence
 CC encoding human beta-NGF operably linked with a DNA sequence capable
 CC of effecting its expression in a recombinant host cell; a replicable
 CC expression vector contg. the DNA; and host cells transformed with
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trip 1. Using
 CC extrn. of natural materials, see e.g. EP-2139.
 XX
 SO Sequence 245 AA;
 Query Match 100.0%; Score 1270; DB 5; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSNLFYTLITAFILGIGQAEPHSSENVPAGHTIPQVMTKLOHSLDTALRRARSAAPAAIA 60
 DB 5 MSNLFYTLITAFILGIGQAEPHSSENVPAGHTIPQVMTKLOHSLDTALRRARSAAPAAIA 64
 QY 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREADTODLDFEVGGAAPFNTRRSK 120

Db 65 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREAADTQDLDPEVGAAPFNRTSRK 124
 Qy 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIKGEVAVLGEVINNSVFKQYFEETKCR 180
 Db 125 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIKGEVAVLGEVINNSVFKQYFEETKCR 184
 Qy 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVCLSRKAVR 240
 Db 185 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVCLSRKAVR 244
 Qy 241 A 241
 Db 245 A 245

RESULT 13 AAR45241

ID AAR45241 standard; Protein; 307 AA.

AC AAR45241;
 DT 20-JUN-1994 (first entry)
 DB Human pre-pro nerve growth factor.
 KB Mature; beta-nerve growth factor; pre-pro portion;
 KW expression; NGF; hNGF; treatment; Alzheimer's Disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..187
 FT Peptide /note= "signal peptide"
 FT Peptide 188..307
 FT Peptide /note= "mature peptide"

FN US5272063-A.

PD 21-DEC-1993.

PP 20-JUN-1989; 89US-0383118.

PR 22-NOV-1988; 88US-0274878.
 PR 20-JUL-1989; 89US-0383118.

PA (SYNT) SYNTAX USA INC.

PI Baecker PA, Barnett JM, Bursztyl-Petegrew H, Chan HM, Nguyen BT,
 Ward C;

DR WPI; 1993-413401/51.

DR N-PSDB; AAO54283.

PT Prodn. of active mature human beta-nerve growth factor in insect
 PT cells - using baculovirus expression system, and potential use of
 PT recombinant hNGF in treatment of Alzheimer's disease
 XX Disclosure; Fig 1; 23pp; English.

CC The sequence is that of human pre-pro nerve growth factor
 CC which was used in a method of producing biologically active
 CC mature human beta-nerve growth factor in insect cells.

SO Sequence 307 AA;

Query Match 99.8%; Score 1267; DB 14; Length 307;
 Best Local Similarity 99.6%; Pred. NO. 4e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMLFTLTITAPLIGIOAEPSHSNVPAGHTIQVHWTKOHLDTPLRARSAPAAIA 60
 Db 67 MSMLFTLTITAPLIGIOAEPSHSNVPAGHTIQVHWTKOHLDTPLRARSAPAAIA 126

Qy 61 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREAADTQDLDPEVGAAPFNRTSRK 120
 Db 127 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREAADTQDLDPEVGAAPFNRTSRK 186
 Qy 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIKGEVAVLGEVINNSVFKQYFEETKCR 180
 Db 187 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIKGEVAVLGEVINNSVFKQYFEETKCR 246
 Qy 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVCLSRKAVR 240
 Db 247 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVCLSRKAVR 306
 Qy 241 A 241
 Db 307 A 307

RESULT 14 AAB67865

ID AAB67865 standard; Protein; 241 AA.

AC AAB67865;
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human polypeptide designated PTMA-8.

KW PTMA; immune deficiency; infection; autoimmune disorder; wound closure;
 KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KW insulin dependent diabetes mellitus; graft-versus-host disease;
 KW autoimmune inflammatory eye disease; gut protection; gut regeneration;
 KW fibrosis; reperfusion injury; systemic cytokine damage.

OS Homo sapiens.

PN WO200123572-A2.

PD 05-APR-2001.

PP 29-SEP-2000; 2000WO-US41035.

PR 30-SEP-1999; 99US-0156745.
 PR 06-OCT-1999; 99US-0158942.
 PR 13-OCT-1999; 99US-0159248.
 PR 06-DEC-1999; 99US-0169344.
 PR 29-JUN-2000; 2000US-0215048.

PA (CURA-) CURAGEN CORP.

PI Prayaga SK, Vernet C, Shinkels RA, Burgess C, Spytek KA;

DR WPI; 2001-273512/28.

DR N-PSDB; AAF60462.

PT Novel polypeptides termed PTMAx, and nucleic acids encoding PTMAx,
 PT useful for detecting and treating diseases caused immune deficiencies -
 XX Claim 1; Page 20-22; 128pp; English.

CC The present sequence represents a PTMA-8 (not defined) polypeptide. The
 CC sequence is derived from clone AL049825. The polypeptide is 26958.5
 CC daltons. PTMA polynucleotides and polypeptides are used in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, the disease selected from a pathology associated with a
 CC PTMA. They may be useful in the treatment of various immune deficiencies
 CC and disorders. These immune deficiencies may be genetic or caused by
 CC viral as well as bacterial or fungal infections or may result from
 CC autoimmune disorders. Autoimmune disorders which may be treated using
 CC PTMA include, for example, connective tissue disease, multiple sclerosis,
 CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation. Guillain-Barre syndrome, autoimmune thyroiditis, insulin
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
 CC and autoimmune inflammatory eye disease. Additionally PTMA may also be
 CC useful to promote better or faster closure of non-healing wounds,
 CC including pressure ulcers, ulcers associated with vascular insufficiency,
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissue, and conditions resulting from
 CC systemic cytokine damage.

XX Sequence 241 AA;

Query Match 99.7%; Score 1266; DB 22; Length 241;
 Best Local Similarity 99.6%; Pred. No. 3.6e-134;
 Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLQHSIDLALRRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLQHSIDLALRRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLPFKKRLRSRVLFSSTQPPREAADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGQTNITVDPRLPFKKRLRSRVLFSSTQPPREAADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSHPITFRGEPFVCDVSVMVGDKTTATDICKKEMVLGEVINNSVFQYFFETKCR 180
 DB 121 RSSHPITFRGEPFVCDVSVMVGDKTTATDICKKEMVLGEVINNSVFQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVER 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVER 240
 QY 241 A 241
 DB 241 A 241

RESULT 15

AA37799 standard; Protein; 307 AA.

AA37799;
 29-SEP-1993 (first entry)

Human NGF.

Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;
 BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;
 central; precursor; nervous system.

Homo sapiens.

Key Location/Qualifiers

Region 1..187

Protein /note= "Prepro region"

188..307

/note= "Mature NGF"

MO310150-A.

27-MAY-1993.

13-NOV-1992; 92MO-US09792.

14-NOV-1991; 91US-0792492.

(AMGR-) AMGEN.

(REG-) REGENERON PHARM INC.

Gies D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;

WPI; 1993-182492/22.

DR N-PSDB; AAQ42571.

XX Eukaryotic expression of neurotrophins - using prepro region of a
 PT different neurotrophin for more efficient post-translational
 PT processing

PS Disclosure; Fig 4; 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein
 CC encoded by this sequence promotes the development of the peripheral
 CC nervous system and also influences the development and maintenance of
 CC specific populations of neurons in the central nervous system. Two
 CC major transcripts from the NGF gene result in a "long" and "short" NGF
 CC prepeptide. The "short" precursor contains a conventional signal
 CC sequence at the N-terminus which flanks the pro-region. The "long"
 CC precursor contains an additional "pro-region" at its N-terminal. No
 CC functional distinction has been elucidated between the "long" and
 CC "short" forms. Characteristics of NGF, such as isoelectric point and
 CC primary structure, are very similar to brain derived neurotrophic
 CC factor (BDNF). The NGF coding sequence may be used in the
 CC construction of a chimeric nucleic acid molecule to encode a prepro-
 CC NGF/BDNF chimera (see also AAQ42568-69).

SQ Sequence 307 AA;

Query Match 99.7%; Score 1266; DB 14; Length 307;
 Best Local Similarity 99.6%; Pred. No. 5.2e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLQHSIDLALRRASAPAAIA 60
 DB 67 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTIPQVHTKLQHSIDLALRRASAPAAIA 126
 QY 61 ARVAGQTNITVDPRLPFKKRLRSRVLFSSTQPPREAADTODLDFEVGAAPFNRTTRSK 120
 DB 127 ARVAGQTNITVDPRLPFKKRLRSRVLFSSTQPPREAADTODLDFEVGAAPFNRTTRSK 186
 QY 121 RSSHPITFRGEPFVCDVSVMVGDKTTATDICKKEMVLGEVINNSVFQYFFETKCR 180
 DB 187 RSSHPITFRGEPFVCDVSVMVGDKTTATDICKKEMVLGEVINNSVFQYFFETKCR 246
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVER 240
 DB 247 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVER 306
 QY 241 A 241
 DB 307 A 307

Search completed: June 6, 2003, 10:49:30
 Job time : 34.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:28 ; Search time 27 Seconds
(without alignments)
1839.161 Million cell updates/sec

Title: US-09-788-188-2

Sequence: 1 MSMLFYTLITFLIGIQAEF.....FIRIDTACVLSRRKAVRA 241

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	99.4	241	4	Q9UKL8
2	1260	99.4	241	4	Q9P2Q8
3	1253	98.8	241	4	Q9P2Q8
4	1244	98.1	241	6	Q9N2P0
5	1243	98.0	241	6	Q9N2P1
6	1242	97.9	241	6	Q9N2P2
7	1127	88.9	217	6	Q9N1B3
8	1033	81.5	224	11	Q91XB4
9	708	55.8	241	13	Q9DBZ9
10	704	55.5	241	13	Q9DBZ9
11	462	36.2	87	6	Q9P2C3
12	459	36.2	87	6	Q9P2C3
13	444.5	35.1	132	11	Q9WU15
14	426	33.6	286	13	Q91988
15	421.5	33.2	241	6	Q9N1B2
16	363	28.6	247	6	Q97759

17	360	28.4	249	11	Q8VHR4	Q8VHR4 mus musculus
18	342.5	27.0	246	13	Q8QG74	Q8QG74 cyclophorus
19	341.5	26.9	246	13	Q8QG76	Q8QG76 japonica sp
20	337.5	26.6	270	13	Q9YH42	Q9YH42 brachydactyl
21	335.5	26.5	246	13	Q8QG75	Q8QG75 phrynosoma
22	334.5	26.4	153	11	Q9CY13	Q9CY13 mus musculus
23	331.5	26.1	177	13	Q918L2	Q918L2 poephila gu
24	318	25.1	247	13	Q8QG77	Q8QG77 tylosotriton
25	294.5	23.2	101	6	Q9TT22	Q9TT22 macaca fusc
26	293	23.1	324	13	Q9XY95	Q9XY95 lampetra fl
27	286	22.6	186	12	Q9JSD9	Q9JSD9 fowipox vir
28	237	18.7	52	6	Q9N1V4	Q9N1V4 equus caball
29	226	17.8	85	6	Q02790	Q02790 macropus fu
30	224	17.7	42	6	Q02802	Q02802 trichosurus
31	220	17.4	85	6	Q03114	Q03114 isodon mac
32	220	17.4	85	6	Q03122	Q03122 tarsipes ro
33	220	17.4	85	6	Q02795	Q02795 ornithorhyn
34	220	17.4	85	6	Q02798	Q02798 petarus br
35	220	17.4	85	6	Q03104	Q03104 cercartetus
36	220	17.4	85	6	Q02792	Q02792 notoryctes
37	220	17.4	85	6	Q03105	Q03105 dasynoides
38	220	17.4	85	6	Q02801	Q02801 tachylosu
39	219	17.3	85	6	Q02803	Q02803 trichosurus
40	211	16.6	42	6	Q02794	Q02794 ornithorhyn
41	209	16.5	42	6	Q02800	Q02800 tachylosu
42	178.5	14.1	186	6	Q9BRJ4	Q9BRJ4 lemur catta
43	178.5	14.1	186	11	Q9NWM1	Q9NWM1 castor cana
44	176.5	13.9	186	6	Q9BF07	Q9BF07 ochotona hy
45	175	13.8	185	6	Q9BFR6	Q9BFR6 talpa alai

ALIGNMENTS

RESULT 1

ID	Q9UKL8	PRELIMINARY	PRT	241 AA.
AC	Q9UKL8			
DT	01-MAY-2000 (TRENBLREL.13, Created)			
DT	01-MAY-2000 (TRENBLREL.13, Last sequence update)			
DT	01-MAR-2002 (TRENBLREL.20, Last annotation update)			
DE	Nerve growth factor B.			
GN	NGFB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9256269; PubMed=10322959;			
RA	Tong Y., Wang H., Chen W.,			
RT	"Cloning and sequencing of the gene for premature beta nerve growth			
RT	factor."			
RL	Chung Kuo Yung Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Tong Y., Wang H.,			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF150960; AAD55975.1;			
DR	HSSP; P01139; 1BET.			
DR	InterPro; IPR002072; NGF.			
DR	Pfam; PF00243; NGF_1.			
DR	PRINTS; PR00268; NGF.			
DR	PRODOM; PD002052; NGF_1.			
DR	SMART; SM00140; NGF_1.			
DR	PROSITE; PS00248; NGF_1;			
DR	PROSITE; PSS0270; NGF_2; 1.			
SO	SEQUENCE 241 AA; 2695 MW; 619DPC65B3BD671 CRC64;			

Query Match 99.4%; Score 1261; DB 4; Length 241;
Best local similarity 99.4%; Pred. No. 7.7e-117;
Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
DB 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
QY 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
DB 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 2

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Q9P208 PRELIMINARY; PRT; 241 AA.
ID 09P208;
AC 09P208;
DT 01-OCT-2000 (Tremblrel. 15, Created).
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Beta-nerve growth factor (fragment).
GN Beta-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB037517; BAA90437.1; -
DR HSP; P01139; ISET.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR NON TER 241
SQ SEQUENCE 241 AA; 26998 MW; D531ED825D96C14 CRC64;

```

Query Match 99.4%; Score 1260; DB 4; Length 241;
 Best Local Similarity 99.2%; Pred. No. 9,7e-117;
 Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
DB 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
QY 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
DB 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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DB 241 A 241

RESULT 3

```

Q96P60 PRELIMINARY; PRT; 241 AA.
ID 096P60;
AC 096P60;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411526; AL05874.1; -
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
DR PROSITE; PS50270; NGF_2; 1.
DR PROSITE; PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 26964 MW; 745216485C21E58 CRC64;

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Query Match 98.8%; Score 1253; DB 4; Length 241;
 Best Local Similarity 98.3%; Pred. No. 4.8e-116;
 Matches 237; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
DB 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARAPAAIA 60
QY 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
DB 61 ARVAGOTRNITVDPRLEFKKRLRSRVLSTOPPREAADTODLDFEVGAAPFSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMVGDKTTATDICKGEVNVLEGVNINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

```

RESULT 4

```

Q9N2F0 PRELIMINARY; PRT; 241 AA.
ID 09N2F0;
AC 09N2F0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Beta-nerve growth factor (fragment).
GN BETA-NGF.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=GORILLA-UI;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037519; BAA90439.1; -

```


DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 FT NON TER 241 241
 SQ SEQUENCE 241 AA; 26915 MW; 6F54D163C384BB34 CRC64;

Query Match 98.1%; Score 1244; DB 6; Length 241;
 Best Local Similarity 98.3%; Pred. No. 3.7e-115;
 Matches 236; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 QY 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

Q9NZF1 PRELIMINARY; PRT; 241 AA.
 ID Q9NZF1 AC Q9NZF1
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Beta-nerve growth factor (Fragment).
 GN BETA-NGF.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 RN NCBI_TaxID=9598;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHIMP-220;
 RA Kitano T., Kobayakawa H., Satou N.;
 RT "Silver Project";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB037518; BAA90438.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 FT NON TER 241 241
 SQ SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match 98.0%; Score 1243; DB 6; Length 241;
 Best Local Similarity 97.9%; Pred. No. 4.7e-115;
 Matches 236; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60

DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 QY 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 6

Q9NZB9 PRELIMINARY; PRT; 241 AA.
 ID Q9NZB9 AC Q9NZB9
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Beta-nerve growth factor (Fragment).
 GN BETA-NGF.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 RN NCBI_TaxID=9600;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORAN-UI;
 RA Kitano T., Kobayakawa H., Satou N.;
 RT "Silver Project";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB037520; BAA90440.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 FT NON TER 241 241
 SQ SEQUENCE 241 AA; 26876 MW; DEC168E7B4E01F15 CRC64;

Query Match 97.9%; Score 1242; DB 6; Length 241;
 Best Local Similarity 97.9%; Pred. No. 5.9e-115;
 Matches 236; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGIAEPHSESNVPAAGHTIPQAHWTQLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLRSPRVLFSTQPPREADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFEETKCR 180
 QY 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 7

Q9N183

ID Q9N183 PRELIMINARY; PRT; 217 AA.

AC Q9N183; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Macaca fuscata (Japanese macaque)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OC NCBI_TaxID=9542;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RX MEDLINE=9270338; PubMed=10340513;

RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in

RT in adult macaque monkeys."

RT J. Comp. Neurol. 408:378-398(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RX Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RA EMBL; AF222682; AAF3790.1; "

DR HSP; P01139; 1BET.

DR InterPro; IPR002072; NGF.

DR Pfam; PF00243; NGF; 1.

DR PRINTS; PR00258; NGF.

DR ProDom; PD002052; NGF; 1.

DR SMART; SM00140; NGF; 1.

DR PROSITE; PS00248; NGF; 1.

DR PROSITE; PS00270; NGF; 2; 1.

FT NON_TER 1

FT NON_TER 217

SQ SEQUENCE 217 AA; 24240 MW; 36A5A2D1DFC8D5C CRC64;

Query Match 88.9%; Score 1127; DB 6; Length 217;

Best Local Similarity 97.7%; Pred. No. 1.3e-103;

Matches 212; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 AFLIGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIAARVAGQTNRI 70

DB 1 AFLIGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIAARVAGQTNRI 60

QY 71 TWDPLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSKSSSHPIFHR 130

DB 61 TWDPLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSKSSSHPIFHR 120

QY 131 GEFVSVCDVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCRDPNPVDSGR 190

DB 121 GEFVSVCDVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCRDPNPVDSGR 180

QY 191 GIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 227

DB 181 GIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 217

RESULT 8

Q91XB4 PRELIMINARY; PRT; 294 AA.

AC Q91XB4; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Similar to nerve growth factor, beta.

GN NGF.

OS Mus musculus (Mouse).

Query Match 55.8%; Score 708; DB 13; Length 241;

Best Local Similarity 59.3%; Pred. No. 4.8e-62;

Matches 143; Conservative 30; Mismatches 58; Indels 10; Gaps 4;

QY 1 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIA 60

DB 67 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIA 126

QY 61 ARVAGQTNITVDRLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSK 120

DB 127 ARVAGQTNITVDRLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSK 186

QY 121 RSSHPIFHRGSEFVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCR 180

DB 187 RSSHPIFHRGSEFVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCR 246

QY 181 DPNVDSGCRGIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 228

DB 247 ASNPVDSGCRGIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 294

RESULT 9

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Salivary Gland;

RA Strausberg R.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011123; AAH11123.1; "

DR MGD; MGI:97321; NGF.

DR InterPro; IPR002072; NGF.

DR Pfam; PF00243; NGF; 1.

DR ProDom; PD002052; NGF; 1.

DR PROSITE; PS00248; NGF; 1; UNKNOWN_1.

DR PROSITE; PS00270; NGF; 2; 1.

SQ SEQUENCE 294 AA; 33246 MW; 9EE7402DAC899229 CRC64;

Query Match 81.5%; Score 1033; DB 11; Length 294;

Best Local Similarity 84.2%; Pred. No. 3.9e-94;

Matches 192; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIA 60

DB 67 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHWTKLOHSIDTALRRASAPAAIA 126

QY 61 ARVAGQTNITVDRLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSK 120

DB 127 ARVAGQTNITVDRLFKKRLRSRVLFTSTOPPEAADTODLDFEVGGAAPFSRTHSK 186

QY 121 RSSHPIFHRGSEFVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCR 180

DB 187 RSSHPIFHRGSEFVSVWVGDKTATDIDIKGRVWLVGEVININNSVFPKQYFETCR 246

QY 181 DPNVDSGCRGIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 228

DB 247 ASNPVDSGCRGIDSKHNSYCTTHTTFYKALTMGKQAAAFIRIDT 294

QY 1 MSMLFTLLTAFLIGIAEPHSESNYPAG---HTIPQVMTLQHSULTALRARSADA 56
1 MSMLCTLLIAFLIGIAWAPKSEEDNPLSPATSDLSDCATHEALTSRNIDQHYA 60
DB 57 AAIWA-RVAGGTRNTVVDRLFKKRLRSPVLPSTQPPREADTDLDPEFGAAPPFR 115
61 PKKAEDEFGSAAITVDPKLFQKRFQSPRVLFSQPPLSRDEQSV-----NANSINR 116
QY 116 TRSKRSSHPHFHGEFVSVDVSVVVDKTTATDICKKRWVVLGEVNNINSVFKQYFF 175
DB 117 NTRAKR-EDHPVHKGEYSVCSVNVVANKTTATDICKGLVTVVVDVNNINSVFKQYFF 175
QY 176 ETKCRDPNVDSGCRGIDSKHNSYCTTHTFEVKALTMGDKQAAWFRIRIDPACVCLSR 235
176 ETKCRNPVPTGCGIDARHNSYCTTNTTFVKALTMGNSQSWFRIRIDACVCLSR 235
QY 236 K 236
DB 236 K 236

RESULT 10

Q90W38 PRELIMINARY; PRT; 241 AA.
ID Q90W38; AC Q90W38;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DB Putative neurotrophic growth factor.
NGF.
OS Bothrops jararacusu (Jararacusu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidogaulia; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=8726;
QX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=VENOM GLAND;
RA Kaishima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
RA Caltara A.C.O., Giglio J.R., Franca S.C.;
RA "Molecular cloning and cDNA sequence of a nerve growth factor
precursor from Bothrops jararacusu venomous gland."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY007318; AAG12169.1;
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
DR PROSITE; PS0270; NGF_2; 1.
SQ SEQUENCE 241 AA, 27161 MW, ACS7F724A6531A8F CRC64;

Query Match 55.5%; Score 704; DB 13; Length 241;
Best Local Similarity 58.9%; Pred. No. 1.2e-61;
Matches 142; Conservative 30; Mismatches 59; Indels 10; Gaps 4;

QY 1 MSMLFTLLTAFLIGIAEPHSESNYPAG---HTIPQVMTLQHSULTALRARSADA 56
1 MSMLCTLLIAFLIGIAWAPKSEEDNPLSPATSDLSDCATHEALTSRNIDQHYA 60
DB 1 MSMLCTLLIAFLIGIAWAPKSEEDNPLSPATSDLSDCATHEALTSRNIDQHYA 60
QY 57 AAIWA-RVAGGTRNTVVDRLFKKRLRSPVLPSTQPPREADTDLDPEFGAAPPFR 115
61 PKKAEDEFGSAAITVDPKLFQKRFQSPRVLFSQPPLSRDEQSV-----DANSINR 116
DB 116 TRSKRSSHPHFHGEFVSVDVSVVVDKTTATDICKKRWVVLGEVNNINSVFKQYFF 175
117 NTRAKR-EDHPVHKGEYSVCSVNVVANKTTATDICKGLVTVVVDVNNINSVFKQYFF 175
QY 176 ETKCRDPNVDSGCRGIDSKHNSYCTTHTFEVKALTMGDKQAAWFRIRIDPACVCLSR 235
176 ETKCRNPVPTGCGIDARHNSYCTTNTTFVKALTMGNSQSWFRIRIDACVCLSR 235
QY 236 K 236

DB 236 K 236

RESULT 11

ID Q9PTC3 PRELIMINARY; PRT; 87 AA.
AC Q9PTC3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DB Beta nerve growth factor (Fragment).
NGF.
OS Cerus elaphus scoticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
NCBI_TaxID=109627;
QX NCBI_TaxID=109627;
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
RA Suttie J.M.;
RA "NGF expression in Antler."
RT Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF145043; AAF17235.1;
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SMO0140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
FT NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA, 9876 MW, 17E06E49A7A0A4 CRC64;

Query Match 36.4%; Score 462; DB 6; Length 87;
Best Local Similarity 36.6%; Pred. No. 3.1e-38;
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 138 SVSVVWGDKTTATDICKKRWVVLGEVNNINSVFKQYFFETKCRDPNPVDSGCRGIDSKHW 197
1 SVSVVWGDKTTATDICKKRWVVLGEVNNINSVFKQYFFETKCRDPNPVDSGCRGIDSKHW 60
DB 1 SVSVVWGDKTTATDICKKRWVVLGEVNNINSVFKQYFFETKCRDPNPVDSGCRGIDSKHW 60
QY 198 NSYCTTHTFEVKALTMGDKQAAWFRIR 224
DB 61 NSYCTTHTFEVKALTMGDKQAAWFRIR 87

RESULT 12

Q9P224 PRELIMINARY; PRT; 87 AA.
ID Q9P224; AC Q9P224;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DB Truncated beta nerve growth factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
QX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95236507; Pubmed=7720122;
RA Li Y., Huang B., Cai L.;
RA "Amplification, cloning and sequencing of beta nerve growth factor
gene in the Chinese population."
RT Chung-Kuo I Hsueh Ko Hsueh Yuan Hsueh Pao 16:334-338 (1994).
RL EMBL; S76884; AAB34114.2;
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.

DR ProdDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON TER 1
 SQ SEQUENCE 87 AA; 9729 MW; 4589E27388FDEB27 CRC64;

Query Match 36.2%; Score 459; DB 4; Length 87;
 Best Local Similarity 94.3%; Pred. No. 6.2e-38;
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 122 SSHPHFHGEFVCSVSWVWGDKTATDICKEMVIGEVNINNSVFOFFETKCRD 181
 DB 1 SSHPHFHGEFVCSVSWVWGDKTATDICKEMVIGEVNINNSVFOFFETKCRD 60

QY 182 PNPVDSGCRGIDSKHNSVCTTHFEV 208
 DB 61 PNPVDSGCRGIDSKHNSVCTTHFEV 87

RESULT 13

Q9WU15 PRELIMINARY; PRT; 132 AA.

DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Nerve growth factor (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jensen H.T., Lehman M.N., Stevens P.J.;
 RT "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104239; AAD21010.1; -
 FT NON TER 1
 FT NON TER 132
 SQ SEQUENCE 132 AA; 14649 MW; 0C36BE6283225DA6 CRC64;

Query Match 35.1%; Score 444.5; DB 11; Length 132;
 Best Local Similarity 74.6%; Pred. No. 2.8e-36;
 Matches 88; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 1 MSMLFYTLITAFILGIOAEPHSESNVPAHGHTIPQVHTKLGHSIDTALRRARAPAAIA 60
 DB 16 MSMLFYTLITAFILGVOAEPYDTSIVPGSDSVPOAHMTKLOHSYDTALRRARAPAGASIA 75
 QY 61 ARVAGQTNITVDPRLFKKRLRSRVLFTSTOPREBADTODLDEVEGGAAPFGRTR 118
 DB 76 ARVAGQTNITVDPRLFKKRLRSRVLFTSTOPREBADTODLDEVEGGAAPFGRTR 132

RESULT 14

Q91988 PRELIMINARY; PRT; 286 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Neurotrophin-6 precursor.
 OS Xiphophorus maculatus (Southern platyfish), and
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 NCBI_TaxID=8083, 8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95059452; PubMed=7969471;

RA Gotz R., Koster R., Winkler C., Raulf F., Lottepeich F., Scharl M.,
 RA Thoenen H.;
 RT "Neurotrophin-6 is a new member of the nerve growth factor family";
 RL Nature 372:266-269(1994).

DR EMBL; U36942; AAA61923.1; -
 DR EMBL; U36925; AAA61922.1; -
 DR EMBL; U36326; AAA61921.1; -
 DR HSSP; P01139; IBER.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProdDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.

DR HSSP; P01139; IBER.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProdDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.

QY 122 SSHPHFHGEFVCSVSWVWGDKTATDICKEMVIGEVNINNSVFOFFETKCRD 181
 DB 1 SSHPHFHGEFVCSVSWVWGDKTATDICKEMVIGEVNINNSVFOFFETKCRD 60

Query Match 33.6%; Score 426; DB 13; Length 286;
 Best Local Similarity 38.6%; Pred. No. 5.1e-34;
 Matches 110; Conservative 31; Mismatches 84; Indels 60; Gaps 10;

QY 8 LITAFILGIOAEPHSESNV-----PAGHTIPQVH-----WTKLQHSIDTALRR 51
 DB 6 LVLLILGVOAVLVMGGILANPGAAHNSAGQCTAAAGLSODQTSYQCHRTTHHTK 65

QY 52 RSAPAA-----IAAVAGQT---RNTVDPRLFKKRLR--SPVLFS--TOPPEAA 98
 DB 66 RTGSAANMQRNTRVIGPSAGSSPDPSPVDPKLPKSHYRSPVVFSEVAPSHDVL 125

QY 99 DTODLDFE-VGGAAPFERTHRSKSSHPHFHGEFVCSVSWVWGDKTATDICKREV 157
 DB 126 DGEYDDEERVGL-----RVKKAHSVTHRGEVSCDSINTW--NKTRATMDSGNEV 177

QY 158 MVIGEVNINNSVFOFFETKCRD-----NVPDSGCRGIDSK 195
 DB 178 TVLSHTVYNNKVKRQKLPYETTCGSPTRSSGIVYGSGRGKQSGKRTGNSGCRGIDSK 237

QY 196 HNSVCTTHHTFVKALTMDSKQAAWRPDIRIDTACVLSRAVVR 240
 DB 238 YNNSHCNTNDIYVSAITVFKQTAWRIRINACVCLSNRSMR 282

RESULT 15

Q9N182 PRELIMINARY; PRT; 241 AA.

DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Neurotrophin-3 (Fragment).
 OS Macaca fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99270338; PubMed=10340513;

RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
 RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys";
 RL J. Comp. Neurol. 408:378-396(1999).

RP SEQUENCE FROM N.A.
 RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;
 RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
 RT their receptor messenger RNAs in monkey rhinal cortex";

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:02 ; Search time 9 seconds
(without alignments)
1110.644 Million cell updates/sec

Title: US-09-788-188-2
Perfect score: 1268
Sequence: 1 MSMTFTLTATFLIGIQAF.....FRIIDTACVLSKAVRRA 241

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	99.8	241	1	NGF_HUMAN
2	1119	88.2	229	1	NGF_PIG
3	1102	86.9	241	1	NGF_RAT
4	1101	86.8	231	1	NGF_BOVIN
5	1091	86.0	241	1	NGF_MOUSE
6	1087	85.7	241	1	NGF_MOUSE
7	1068	84.2	241	1	NGF_CAVRO
8	783.5	61.8	241	1	NGF_PRAWA
9	768	60.6	231	1	NGF_CHICK
10	671.5	53.0	243	1	NGF_BUNMU
11	484	38.2	117	1	NGF_DABRR
12	481.5	38.0	194	1	NGF_XIPMA
13	476.5	37.6	257	1	NT3_HUMAN
14	469	37.0	260	1	NT3_XENLA
15	468.5	36.9	257	1	NT3_FELCA
16	467	36.8	258	1	NT3_MOUSE
17	466.5	36.8	257	1	NT3_CHICK
18	466	36.8	258	1	NT3_RAT
19	459.5	36.2	233	1	NT7_BRABR
20	449.5	35.4	116	1	NGF_NAJNA
21	445.5	35.1	116	1	NGF_NAJNA
22	372.5	29.4	140	1	NT7_CYPCA
23	365	28.8	247	1	BDNF_HUMAN
24	364	28.7	249	1	BDNF_RAT
25	363	28.6	255	1	BDNF_PIG
26	362	28.5	247	1	BDNF_CAVRO
27	361	28.5	247	1	BDNF_URSLR
28	361	28.5	247	1	BDNF_MOUSE
29	360	28.4	249	1	BDNF_MOUSE
30	358.5	28.3	252	1	BDNF_PIG
31	350	27.6	247	1	BDNF_FELCA
32	348.5	27.5	248	1	BDNF_BOVIN
33	347.5	27.4	246	1	BDNF_CHICK

ALIGNMENTS

34	338	26.7	236	1	NT4_XENLA	P24727 xenopus lae
35	336.5	26.5	270	1	BDNF_CYPCA	O90322 cyprinus ca
36	335	26.4	269	1	BDNF_XIPMA	Q02193 xiphophorus
37	332.5	26.2	210	1	NT5_HUMAN	P34131 rattus norv
38	325.5	25.7	209	1	NT5_RAT	Q06225 macaca mla
39	323.5	25.5	114	1	BDNF_MACMU	P25432 xenopus lae
40	307.5	24.3	114	1	BDNF_XENLA	P34133 homo sapien
41	230	18.1	257	1	NT6B_HUMAN	P34132 homo sapien
42	227	17.9	257	1	NT6A_HUMAN	P34134 homo sapien
43	226	17.8	186	1	NT6G_HUMAN	P25428 vipera lebe
44	190	15.0	42	1	NGF_VIPLE	Q95150 cervus elap
45	139	11.0	154	1	NT3_CEREL	

RESULT 1
ID NGF_HUMAN STANDARD, PRT, 241 AA.
AC P0138;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RX MEDLINE=83244969; PubMed=6688123;
RA Ullrich A., Gray A., Berman C., Dull T.J.;
RT "Human beta-nerve growth factor gene sequence highly homologous to
RL that of mouse.";
RL Nature 303:821-825(1983).
RN [2]
RX MEDLINE=84206565; PubMed=6327169;
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
RT "Sequence homology of human and mouse beta-NGF subunit genes.";
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
RN [3]
RX MEDLINE=90326556; PubMed=2374737;
RA Borsani G., Pizzuti A., Ruggeri E.I., Falini A., Siland V.,
RT "CDNA sequence of human beta-NGF.";
RL Nucleic Acids Res. 18:4020-4020(1990).
RN [4]
RX MEDLINE=178-219 FROM N.A.
RA TISSUE=Leukocyte;
RC TISSUE=Leukocyte;
RX MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RN [5]
RX MEDLINE=6845-858(1991).
RA "FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
-1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
-1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: VO1511; CAA24755.1;
DR EMBL: M21062; AA55931.1;
DR EMBL: X52599; CAA36832.1;
DR PIR: A01399; NGHDM.
DR PIR: S10253; S10253.
DR HSSP: P01139; 1BET.
DR Genem; HGNC:7808; NGFB.
DR MIM: 162030;
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR Growth factor; Signal.
KM SIGNAL.
FT PROPEP 1 121
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SQ SEQUENCE 241 AA; 26987 MW; CFIIDB4DCB736B0F CRC64;

Query Match 99.8%; Score 1265; DB 1; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.3e-112;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSMTPLYTLTAFLGIGQEPHSESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIA 60
DB 1 MSMTPLYTLTAFLGIGQEPHSESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIA 60
QY 61 ARVAGQTNITVDPRLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSK 120
DB 61 ARVAGQTNITVDPRLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSK 120
QY 121 RSSHPIFRHGEFVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSHPIFRHGEFVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCR 180
QY 121 RSSHPIFRHGEFVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSHPIFRHGEFVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNVDSGCGIGIDSKHNSVCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 240
DB 181 DPNVDSGCGIGIDSKHNSVCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 240
QY 241 A 241
DB 241 A 241

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RESULT 2
NGF_PIG STANDARD; PRT; 229 AA.

AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RX MEDLINE=94313891; PubMed=8039422;
RA Labbb-Mansais Y., Mellink C., Yerie M., Gellin J.,
RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
RT consensus sequence conserved among species.",
RL Cytogenet. Cell Genet. 67:120-125 (1994).

-1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.
-1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
-1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: L31898; AAA21301.1;
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF_2; 1.
KM Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 6
FT PROPEP 7 109
FT CHAIN 110 229
FT DISULFID 124 189
FT DISULFID 167 217
FT DISULFID 177 219
FT CARBOHYD 57 57
FT CARBOHYD 102 102
FT CARBOHYD 154 154
SQ SEQUENCE 229 AA; 25275 MW; FE8890771CEA3189 CRC64;

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Query Match 88.2%; Score 1119; DB 1; Length 229;
Best Local Similarity 92.1%; Pred. No. 8.2e-99;
Matches 211; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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QY 13 LIGIOEPHSESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIAARVAGQTNITV 72
DB 1 LIGIOEPHSESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIAARVAGQTNITV 72
QY 73 DPLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSKSSSHPIFRGE 132
DB 73 DPLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSKSSSHPIFRGE 132
QY 61 DPLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSKSSSHPIFRGE 120
DB 61 DPLFKKRLRSRPRVLFSTQPREAADTODLDFEVGAAAPFSRTRSKSSSHPIFRGE 120
QY 133 FSVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCGI 192
DB 133 FSVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCGI 192
QY 121 FSVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCGI 180
DB 121 FSVCSVSVMVDKTTATDIDKEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCGI 180
QY 193 DSKHNSVCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 241
DB 193 DSKHNSVCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 241

```

RESULT 3
NGF_RAT STANDARD; PRT; 241 AA.

AC P23427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=3184206;

RA Whitehead S.R., Friedman P.L., Lathammar D.G., Persson H.,
 RA Gonzalez-Carvajal M., Holets V.R.,
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the
 RT adult hippocampus";
 RL J. Neurosci. Res. 20:403-410(1998).
 RN [2]
 RP SEQUENCE OF 178-219 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=9122573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.,
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary";
 RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 DR EMBL; M36589; AAA1697.1; ALT_INIT.
 DR HSBP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR KMW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 FT CARBOHYD 166 166
 FT SEQUENCE 241 AA; 27009 MW; 665F42371563213D CRC64;
 SO
 Query Match 86.9%; Score 1102; DB 1; Length 241;
 Best Local Similarity 85.4%; Pred. No. 3.6e-97;
 Matches 205; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 Oy 1 MSMLFYTLITLFLGIQAEPPHSESNVPAHGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 Db 1 MSMLFYTLITLFLGIQAEPPHSESNVPAHGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 Oy 61 ARVAGGTNTIVDPLFKKRLRSPRLVPSPTOPREAADTQDLDEVGGAAPFSTHRSK 120
 Db 61 ARVAGGTNTIVDPLFKKRLRSPRLVPSPTOPREAADTQDLDEVGGAAPFSTHRSK 120
 Oy 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDICKGRVAVLVGEVNNINSVFQYFETCKR 180
 Db 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDICKGRVAVLVGEVNNINSVFQYFETCKR 180
 Oy 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDICKGRVAVLVGEVNNINSVFQYFETCKR 180
 Db 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDICKGRVAVLVGEVNNINSVFQYFETCKR 180
 Oy 181 DPNPDSGCRGIDSGHNSYCTTTTFYKALTMGKQAAAFRIRIDTACVCLSKAVAR 240
 Db 181 DPNPDSGCRGIDSGHNSYCTTTTFYKALTMGKQAAAFRIRIDTACVCLSKAVAR 240
 Oy 181 APNPVSESGCRGIDSGHNSYCTTTTFYKALTMGKQAAAFRIRIDTACVCLSKAVAR 240
 Db 181 APNPVSESGCRGIDSGHNSYCTTTTFYKALTMGKQAAAFRIRIDTACVCLSKAVAR 240
 RESULT 4
 NGF_BOVIN STANDARD; PRT; 231 AA.

AC P13600; O18969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (beta-NGF) (fragment).
 OS NGF.
 GN Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97430845; PubMed=9284944;
 RA Eideque C., Laurent P., Hayes H., Rodellar C., Levezuel H.,
 RT "Assignment of the beta-nerve growth factor (NGF) to bovine
 RT chromosome 3 band q23 by in situ hybridization";
 RL Cytogenet. Cell Genet. 77:306-307(1997).
 RN [2]
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE=8630647; PubMed=2427334;
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.,
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF";
 RL EMBO J. 5:1489-1493(1986).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL; Y09566; CA970759.1; -
 DR EMBL; M26809; AAA30666.1; -
 DR PIR; A26312; A26312.
 DR HSBP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR KMW Growth factor; Signal.
 FT SIGNAL 1 1
 FT PROPEP 9 111
 FT CHAIN 112 231
 FT DISULFID 126 191
 FT DISULFID 169 219
 FT DISULFID 179 221
 FT CARBOHYD 156 156
 FT CARBOHYD 118 118
 FT CARBOHYD 161 161
 FT CONFLICT 230 231
 FT CONFLICT 231 231
 FT SEQUENCE 231 AA; 25437 MW; 01605099291A4A8C CRC64;
 SO
 Query Match 86.8%; Score 1101; DB 1; Length 231;
 Best Local Similarity 90.3%; Pred. No. 4.2e-97;
 Matches 204; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 Oy 11 AFLLGIQAEPPHSESNVPAHGHTIPQVHTKLOHSIDTLARRASAPAAIAARVAGGTNTI 70
 Db 11 AFLLGIQAEPPHSESNVPAHGHTIPQVHTKLOHSIDTLARRASAPAAIAARVAGGTNTI 70

Db 1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLQHSIDTALRRASAPAPAA 60

Qy 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFVGAAPSRTRSK 120

Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFVGAAPSRTRSK 120

Qy 121 RSSHPHIFRGEFSCDSVSVWVGDKTTATDIDKGEVMTLGEVNNINSVFQYFFETKCR 180

Db 121 RSSHPHIFRGEFSCDSVSVWVGDKTTATDIDKGEVMTLGEVNNINSVFQYFFETKCR 180

Qy 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRIRIDTACVCLSRKAVR 240

Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRIRIDTACVCLSRKAVR 240

RESULT 6

NGF_CAVPO STANDARD, PRT, 241 AA.

AC P19093;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Beta-nerve growth factor precursor (Beta-NGF).

GN NGFB.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Cavia.

OX NCBI_TaxId=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RL MEDLINE=89177243; PubMed=2926397;

RA Schwarz M.A., Fisher D., Bradshaw R.A., Isaacson P.J.;

RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig prostate gland."

RL J. Neurochem. 52:1203-1209(1989).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.

CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

DR PIR, J10097; J10097.

DR HSP; P01139; 18RT.

DR InterPro; IPR002072; NGF.

DR Pfam; PF00243; NGF.

DR PRINTS; PR00268; NGF.

DR Prodom; PD002052; NGF.

DR SMART; SM00140; NGF_1.

DR PROSITE; PS00248; NGF_1.

DR PROSITE; PS50270; NGF_2; 1.

KW Growth factor; Signal.

FT SIGNAL 1

FT PROPEP 18

FT CHAIN 122

FT DISULFID 136

FT DISULFID 179

FT DISULFID 189

FT CARBOHYD 69

FT CARBOHYD 114

FT CARBOHYD 241

SEQ 241 AA; 26621 MW; 2F4E26B197804B84 CRC64;

Query Match 85.7%; Score 1087; DB 1; Length 241;

Best Local Similarity 85.8%; Pred. No. 9.4e-96;

Matches 206; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLQHSIDTALRRASAPAPAA 60

Db 1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLQHSIDTALRRASAPAPAA 60

Qy 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFVGAAPSRTRSK 120

Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFVGAAPSRTRSK 120

Qy 121 RSSHPHIFRGEFSCDSVSVWVGDKTTATDIDKGEVMTLGEVNNINSVFQYFFETKCR 180

Db 121 RSSHPHIFRGEFSCDSVSVWVGDKTTATDIDKGEVMTLGEVNNINSVFQYFFETKCR 180

Qy 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRIRIDTACVCLSRKAVR 240

Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRIRIDTACVCLSRKAVR 240

RESULT 7

NGF_PRANA STANDARD, PRT, 241 AA.

AC P20675;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Beta-nerve growth factor precursor (Beta-NGF).

GN NGFB.

OS Pracomys natalensis (African soft-furred rat) (Mastomys natalensis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mastomys.

OX NCBI_TaxId=10112;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=89172070; PubMed=3234767;

RA Fahnestock M., Bell R.A.;

RT "Molecular cloning of a cDNA encoding the nerve growth factor precursor from Mastomys natalensis."

RL Gene 69:257-264(1988).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.

CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC -----

DR EMBL; M22748; AAA40599.1; ALT_INIT.

DR PIR; J10343; NGRTBA.

DR HSP; P01139; 18RT.

DR InterPro; IPR002072; NGF.

DR Pfam; PF00243; NGF.

DR PRINTS; PR00268; NGF.

DR Prodom; PD002052; NGF.

DR SMART; SM00140; NGF_1.

DR PROSITE; PS00248; NGF_1.

DR PROSITE; PS50270; NGF_2; 1.

KW Growth factor; Signal.

FT SIGNAL 1

FT PROPEP 18

FT CHAIN 122

FT DISULFID 136

FT DISULFID 179

FT DISULFID 189

FT CARBOHYD 69

FT CARBOHYD 114

FT CARBOHYD 241

SEQ 241 AA; 27035 MW; 8BFB207A1FEB287 CRC64;

Query Match 84.2%; Score 1068; DB 1; Length 241;

Best Local Similarity 82.9%; Pred. No. 5.9e-94;

Matches 199; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLQHSIDTALRRASAPAPAA 60

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Db 1 MSMLFTLLTALLIGVQAEPTDLSNLPBGDSVPEAHMTLQSLDTPALRASAPAPAPTA 60
Qy 61 ARVAGTNRITVDPRLFKKRLRSRVLFPSTQPPREADTODLPDEVGAAFPSTHRSK 120
Db 61 ARVAGTNRITVDPRLFKKRLRSRVLFPSTQPPREADTODLPDEVGAAFPSTHRSK 120
Qy 121 RGSHPHFRKGEPSVDSVSVWVGDKTTATDICKGEVWMLGSEVNNINSVFKQYFPEYKCR 180
Db 121 RGSHPHFRKGEPSVDSVSVWVGDKTTATDICKGEVWMLGSEVNNINSVFKQYFPEYKCR 180
Qy 181 DENPVDGSGRGIDSKHMSYCTTTHFVYALTMGDKOAMRIRIDTACVCLSKAVR 240
Db 181 AANPVSQSGRGIDSKHMSYCTTTHFVYALTMGDKOAMRIRIDTACVCLSKAVR 240

RESULT 8
NGF_CHICK STANDARD; PRT; 243 AA.
AC POS300; 1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86300646; PubMed=3017695;
RA Eberdahl T., Lathimmar D., Persson H.;
RT "Structure and expression of the chicken beta nerve growth factor
RT gene."
RL EMBL J. 5:1483-1487(1986).
RN [2]
RP SEQUENCE OF 118-243 FROM N.A.
RA MEDLINE=86248129; PubMed=3720959;
RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
RA Auffray C.;
RT "Molecular cloning of the avian beta-nerve growth factor gene:
RT transscription in brain."
RL PNAS Lett. 203:82-86(1986).
RN [3]
RP SEQUENCE OF 121-243 FROM N.A.
RA MEDLINE=86300647; PubMed=2427334;
RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF."
RL EMBL J. 5:1469-1493(1986).
RN [4]
RP SEQUENCE OF 181-222 FROM N.A.
RA MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
RN [5]
RP MAINTENANCE OF THE NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
RP STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
RP EMBRYONIC SENSORY NEURONS.
RN [6]
RP -1 SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
RN [7]
RP -1 SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
RN [8]
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CC EMBL; X04003; CAA27633.1; ALT_INT.
DR EMBL; X04067; CAA27703.1; -.
DR EMBL; M26810; AAA48984.1; -.
DR PIR; A24857; A24857.
DR PIR; A26311; A26311.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; P002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
KV Growth factor; Signal_1.
FT SIGNAL 1 22
FT PROPEP 23 125
FT CHAIN 126 243
FT DISULFID 139 204
FT DISULFID 182 232
FT DISULFID 192 234
SQ SEQUENCE 243 AA; 27138 MW; 74C306CB207DA07 CRC64;

Query Match 61.8%; Score 783.5; DB 1; Length 243;
Best Local Similarity 64.5%; Pred. No. 5.2e-67;
Matches 160; Conservative 21; Mismatches 48; Indels 19; Gaps 6;

Qy 1 MSMLFTLLTALLIGVQAEPTDLSNLPBGDSVPEAHMTLQSLDTPALRASAPAPTA 56
Db 5 MSMLYTLTLLAFLGTAAPKSRVLPSTQPPVSKRGSTGF-LSGAV 57
Qy 57 AAIARVA-----GQNRITVDPRLFKKRLRSRVLFPSTQPPREADTODLPDEVGAA 111
Db 58 TT-HGRANMPDGDIEDINIMDQNFKKKRRSRVLPSTQPPVSKRGSTGF-LSGAV 115
Qy 112 PFSRHSKSSSHPIFRGEPSVDSVSVWVGDKTTATDICKGEVWMLGSEVNNINSVFK 171
Db 116 SLNRTRATKR-TAPVLRGEPSVDSVSVWVGDKTTATDICKGEVWMLGSEVNNINSVFK 174
Qy 172 QYFETCRDPNPNPDSGCRGIDSKHMSYCTTTHFVYALTMGDKOAMRIRIDTACVC 231
Db 175 QYFETCRDPNPNPDSGCRGIDSKHMSYCTTTHFVYALTMGDKOAMRIRIDTACVC 234
Qy 232 VLSRKAAR 239
Db 235 VLSRKSAR 242

RESULT 9
NGF_XENLA STANDARD; PRT; 231 AA.
ID NGF_XENLA
AC P1617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinalli B., Pierandrei-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RP SEQUENCE OF 170-211 FROM N.A.
RN T18UVE-Liver;
RX MEDLINE=91222573; PubMed=2025430;

```

RA Hallboeck F., Ibanez C.F., Persson H.
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.",
 CC Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC EMBL, X55716; CAA39249.1; ALT_INIT.
 CC PIR, S1481; S1481.
 CC HSSP, P01139; 1BET.
 CC InterPro, IPR002072; NGF.
 CC Pfam, PF00243; NGF_1.
 CC PRINTS, PR00268; NGF.
 CC ProDom, PD002052; NGF_1.
 CC SMART, SM00140; NGF_1.
 CC PROSITE, PS00248; NGF_1; 1.
 CC PROSITE, PS50270; NGF_2; 1.
 CC Growth factor: Signal.
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 114
 CC FT CHAIN 115 231
 CC FT DISULFID 128 193
 CC FT DISULFID 171 221
 CC FT DISULFID 181 223
 CC FT CARBOHYD 63 63
 CC FT CARBOHYD 107 107
 CC FT CARBOHYD 158 158
 CC SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;
 SQ
 Query Match 60.6%; Score 768; DB 1; Length 231;
 Best Local Similarity 63.2%; Pred. No. 1.4e-65;
 Matches 153; Conservative 28; Mismatches 41; Indels 20; Gaps 6;
 QY 1 MSMLFYTLITFLIGIOAPHSSESNVPAGHT-----IP-QVHTK-LQHSIDTALRRASA 54
 DB 1 MSMLFYTLITFLIGIOAPHSSESNVPAGHT-----IP-QVHTK-LQHSIDTALRRASA 49
 QY 55 PAAAIARVAGOTRNITVDPRILFKKRLRSRVLSTOPPREADTDLDPEVGGAAPFS 114
 DB 50 -HGKLEAKPEPVFRVITVDPKLFRKRFSPRVLFSTPPPLSEDFOLEY-LDDEBSLN 107
 QY 115 RTHSKSSSSHPITFRGEPVCDVSVMVGDTTADIKKKEVMVLGVNINNSVFKQYF 174
 DB 108 KTIIRAKR-TVHPVHKGEYSVCDVSVMVGEXTKATDIKKEVTVLGVNINNSVFKQYF 166
 QY 175 PETCRDPNPVDSGGRGIDSKHNSYCTTHTFVKALTMDSKOAMRIRIDTACVCL 234
 DB 167 PETCRDPKPVSSGGRGIDAKHNSYCTTHTFVVALTMDSKOAMRIRIDTACVCL 226
 QY 235 RK 236
 DB 227 RK 228
 RESULT 10
 ID NGF_BUNMU STANDARD; PRT; 243 AA.
 AC P34128;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 CC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Elapidae; Bungarinae; Bungarus.
 CC NCBI_TaxID=8616;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RC TISSUE=Venom gland;
 CC RX MEDLINE=93192074; PubMed=7916740;
 RA Danse J.M., Garnier J.M.;
 RT Molecular cloning of a cDNA encoding a nerve growth factor precursor
 RL from the krait, Bungarus multicinctus.",
 CC Growth Factors 8:77-86(1993).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL, S56212; AAB25729.1; -.
 CC HSSP, P01139; 1BET.
 CC InterPro, IPR002072; NGF.
 CC Pfam, PF00243; NGF_1.
 CC PRINTS, PR00268; NGF.
 CC ProDom, PD002052; NGF_1.
 CC SMART, SM00140; NGF_1.
 CC PROSITE, PS00248; NGF_1; 1.
 CC PROSITE, PS50270; NGF_2; 1.
 CC Growth factor: Signal.
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 125
 CC FT CHAIN 126 243
 CC FT DISULFID 139 204
 CC FT DISULFID 182 232
 CC FT DISULFID 192 234
 CC SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;
 SQ
 Query Match 53.0%; Score 671.5; DB 1; Length 243;
 Best Local Similarity 56.1%; Pred. No. 2.1e-56;
 Matches 138; Conservative 29; Mismatches 62; Indels 17; Gaps 5;
 QY 1 MSMLFYTLITFLIGIOAPHSSESNVPAG-----HTIQVHTK-LQHSIDTALRRASA 56
 DB 1 MSMLFYTLITFLIGIOAPHSSESNVPAG-----HTIQVHTK-LQHSIDTALRRASA 60
 QY 57 AAIARVAGOTRNITVDPRILFKKRLRSRVLSTOPPREADTDLDPEVGGAAP 112
 DB 61 PKSEDDDELGAANIITVDPKLFRKRFSPRVLFSTPPPLSDEGVKFLDE----- 114
 QY 113 FSRTHRS--KSSSHPIFRHGEPSVCDVSVMVGDTTADIKKKEVMVLGVNINNSVF 170
 DB 115 -DTLRNIMANNENHPVHNGEHSVCDISVVMVTKKATDIGNTVTVAVDVANNEVY 173
 QY 171 KQYFEETCRDPNPVDSGGRGIDSKHNSYCTTHTFVKALTMDSKOAMRIRIDTACV 230
 DB 174 KQYFEETCRDPNPVDSGGRGIDSKHNSYCTTHTFVKALTMDSKOAMRIRIDTACV 233
 QY 231 CVLSRK 236
 DB 234 CVLSRK 239

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RESULT 11
NGF_DABRR
ID NGF_DABRR STANDARD; PRT; 117 AA.
AC P30894;
DT 01-JUL-1993 (Rel. 26, Created)
RT 01-JUL-1993 (Rel. 26, Last sequence update)
DB 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF)
OS Dabola russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabola.
OX NCBI_TaxId=31159;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
the venom of Vipera russelli russelli";
RL Biochim. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMERSONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF; 2; 1.
KW Glycoprotein; Growth factor.
FT DISULFID 12 77
FT DISULFID 55 105
FT DISULFID 65 107
FT CARBOHYD 21 21
SQ SEQUENCE 117 AA; 13283 MW; A64559C5FBC11F66 CRC64;

Query Match
Best Local Similarity 74.1%; Score 484; DB 1; Length 117;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 125 HPIFHGEFVSVDVWGDKTTATDIDGKRVWVIGRVNINNSVFKOYFEFTKCRDPNP 184
DB 1 HPIFHGEFVSVDVWGDKTTATDIDGKRVWVIGRVNINNSVFKOYFEFTKCRDPNP 60

QY 185 VDSGCGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRK 236
DB 61 VDSGCGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRK 112

RESULT 12
NGF_XIPMA
ID NGF_XIPMA STANDARD; PRT; 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
RT 01-FEB-1994 (Rel. 28, Last sequence update)
DB 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoceratopterygii; Teleostei; Euteleostei; Neocentropomus;
OC Acanthomorphia; Acanthopterygii; Perciformes; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxId=8083;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92333301; PubMed=1629719;
RA Gocz R., Kaulf F., Scharf M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
structure and function than nerve growth factor during vertebrate
evolution";
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMERSONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
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CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR HSB; X59941; CAA42566.1; -.
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS50270; NGF; 2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 30
FT PROPEP 31 79
FT CHAIN 80 194
FT DISULFID 90 155
FT DISULFID 133 183
FT DISULFID 143 185
SQ SEQUENCE 194 AA; 21596 MW; 0369E0FA51147AE CRC64;

Query Match
Best Local Similarity 59.3%; Score 481.5; DB 1; Length 194;
Matches 99; Conservative 14; Mismatches 39; Indels 15; Gaps 3;

QY 71 TVDRLFLFKRLRSPRVLFSTQPREADTDGLDFEVGAAPFSTRHSKSSHPFR 130
DB 40 TVDRLFLFKRLRSPRVLFSTQPREADTDGLDFEVGAAPFSTRHSKSSHPFR 84

QY 131 GEFVSVDVWGDKTTATDIDGKRVWVIGRVNINNSVFKOYFEFTKCRDPNPVDSGR 190
DB 85 GEFVSVDVWGDKTTATDIDGKRVWVIGRVNINNSVFKOYFEFTKCRDPNPVDSGR 144

QY 191 GIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRK 237
DB 145 GIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRK 191

RESULT 13
NT3_HUMAN
ID NT3_HUMAN STANDARD; PRT; 257 AA.
AC P20783;
DT 01-FEB-1991 (Rel. 17, Created)
RT 01-FEB-1991 (Rel. 17, Last sequence update)
DB 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RA MEDLINE=90262727; PubMed=2344409;
 RA Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Laramee G.R., Nikolic K., Winalow J.W.;
 RT "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773(1990).
 (2)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91045937; PubMed=2236018;
 RA Jones K.R., Reichardt L.F.;
 RT "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).
 (3)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90306351; PubMed=2365067;
 RA Katsuno Y., Yoshimura K., Nakahama K.;
 RT "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RL FEBS Lett. 266:187-191(1990).
 (4)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91363561; PubMed=1889806;
 RA Malsompierre P.C., le Beau M.M., Espinosa R. III, IP N.Y.,
 RA Belluscio L., de la Monte S.M., Siquinto S., Furch M.E.,
 RA Yancopoulos G.D.;
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RL Genomics 10:558-568(1991).
 (5)
 RP SEQUENCE OF 194-236 FROM N.A.
 RA TISSUE=Leukocyte;
 RX MEDLINE=9122573; PubMed=2025430;
 RX Hallboeck F., Ibanez C.F., Persson H.;
 RA "Evolutionary studies of the nerve growth factor family reveal a
 RA novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 (6)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=95217877; PubMed=7703225;
 RX Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;
 RA "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RA heterodimer.";
 RL Biochemistry 34:4139-4146(1995).
 (7)
 RP VARIANT GLU-76.
 RX MEDLINE=95251647; PubMed=7733919;
 RX Hattori M., Nanko S.;
 RA "Association of neurotrophin-3 gene variant with severe forms of
 RA schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518(1995).
 (8)
 RP VARIANT GLU-76.
 RX MEDLINE=96253892; PubMed=8925252;
 RX Aizawa T., Takekoshi K., Itokawa M., Hamaguchi H., Tori M.;
 RA "Failure to find associations of the CA repeat polymorphism in the
 RA first intron and the Gly-63/Glu-63 polymorphism of the neurotrophin-3
 RA gene with schizophrenia.";
 RL Psychiatr. Genet. 6:13-15(1996).
 (9)
 RP FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 RP PROPRIOCEPTIVE SENSORY NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 CC thought to be associated with severe forms of schizophrenia. This
 CC does not seem to be the case.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL; X53655; CAA37703.1; -
 DR EMBL; M37763; AAA59953.1; -
 DR EMBL; M61180; AAA63231.1; -
 DR PIR; JH0141; JH0141.
 DR PIR; A36208; A36208.
 DR PIR; S10719; S10719.
 DR PIR; C40304; C40304.
 DR PDB; 1BND; 04-APR-96.
 DR PDB; 1B8K; 09-FEB-99.
 DR Genew; HGNC:8023; NTF3.
 DR MIM; 162660; -
 DR InterPro; IPR002400; GF_cybknot.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF_1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF_1.
 DR SMART; SM00140; NGF_1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 DR Growth factor; Signal; Polymorphism; 3D-structure.
 DR SIGNAL; 1; 16
 FT PROPEP 17 138
 FT CHAIN 139 257 NEUTROPHIN-3.
 FT DISULFID 152 217
 FT DISULFID 195 246
 FT DISULFID 205 248
 FT CARBOHYD 131 131
 FT VARIANT 76 76
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT G->E.
 FT /ftid=VAR_012084.
 SQ SEQUENCE 257 AA; 29354 MW; 39A5BB328E25E03 CRC64;
 Query Match 37.6%; Score 476.5; DB 1; Length 257;
 Best Local Similarity 40.3%; Pred. No. 6,7e-38;
 Matches 106; Conservative 38; Mismatches 88; Indels 31; Gaps 6;
 QY 1 MSMLFTLTITAFILGIGIAQEPHSBSNPAGHTIPQV-----HWTKLOHSLD 45
 DB 1 MSILFYIFPLAAYLRGIGGNMDDQSLPBDLSNLSIITLQADILKNTLSQMWVDKENYO 60
 QY 46 TALRRA-----RSAPAAIAARVAGQTNITVDPRLFK-KERLNSPRVLFSTQPPREA 97
 DB 61 STLPKAPREPREGKAGKAFQV-----IMDELRLAQGRNYSRVLDSSTLEP 114
 QY 98 ADYODLDFEYGAAPFSRTSRSSSHPIFRGERSVCDVSVMWGDKTATDINGEV 157
 DB 115 PPLYMEDVGSPPVNNRTSRKRYAEHK-SHREGVSCDSBSLWYTDKSSAIDIRHQV 173
 QY 158 MVLGEVNNNSVVKQYFEETKCRDPNPVDSGCGGIDSKHNSVCTTHFVKALTM-D-GK 216
 DB 174 TVLGEITGNSPVKQYFETRCARPVKNGCKGIDKHMNSOCKTSQYVRLTSENNK 233
 QY 217 QAARFIRIDYACVYLSRRKAVR 239
 DB 234 LVGRWIRIDTSCVCAISRIGR 256
 RESULT 14
 NT3_XENLA STANDARD; PRT; 260 AA.
 ID NT3_XENLA
 AC P5135;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve
 DE growth factor 2) (NGF-2).
 OS Xenopus laevis (African clawed frog).
 OC Bakayoca; Melzosa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

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OK NCBI_TaxID=8355;
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=97252639; PubMed=9096131;
RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
RT "Activity-dependent expression of NF-3 in muscle cells in culture:
RL implications in the development of neuromuscular junctions.";
RN J. Neurosci. 17:2947-2958(1997).
(2)
RP SEQUENCE OF 197-217 FROM N.A.
RC TISSUE=Liver; PubMed=2025430;
RX MEDLINE=9122573;
RA Hallboeck P., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RN Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: U27576; AAB17723.1; -
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00438; GF_CYSKNOT.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR KEGG: K04400; NGF_1.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 141
FT CHAIN 142 260 NEUROTROPHIN-3.
FT DISULFID 155 220 BY SIMILARITY.
FT DISULFID 198 249 BY SIMILARITY.
FT DISULFID 208 251 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5EA93CC5 CRC64;

Query Match 37.0%; Score 469; DB 1; Length 260;
Best Local Similarity 41.2%; Pred. No. 3.5e-37;
Matches 107; Conservative 37; Mismatches 94; Indels 22; Gaps 7;

1 MSMLFTLTITAFILGIGIAEPHSESNVPAGH-----TIQVMTK---LQSLDPAKRA 51
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1 MSILFTVMTFLPICGHATMDKRNLPKSLQADLLKKNKSKQVDTKRNQ 60
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52 KAAPAAIAARVAGQTRN-----ITVDPRLF--KGRILSPRYLSTQPPREADTQ 101
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 STLPKQQLLDLDGDNDKQDFQVSLAEALVKQKQKRYKSPRYLSDSLPLPPPLY 120
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102 DLDPEVGAAFP--STHRSKRSSSHPIFRGGEPSVCDVSVAWGDKTTATDICKKXENVL 160
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121 LMDVDYIGHSITVNNNRISRRKRFARHK--GRGYSVCDSESLVWTMMNAIDIRGHQVTVL 179
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
161 GEVNTINSVKQYFFETKCRDPNPVDSGCGIGDSKHMNSYCTTHHTFYKALTMQ--GKQAA 219
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
180 GEIKGNSPVKQYFETRCKEARPYANGCGRIDDGHMNSQCTISQTYVALTSNNKXWG 239
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 220 WAFIRIDTACVCLSKAVR 239
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DB 240 WFWIRIDTSCVCLSKRIGR 259

RESULT 15
ID NT3_FELCA STANDARD; PRT; 257 AA.
AC 09TSY2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neutrotrophin-3 precursor (NT-3) (Neutrotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20211727; PubMed=10745216;
RA Lein E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RT development.";
J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF192538; AAF03424.1; -
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR KEGG: K04400; NGF_1.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 138
FT CHAIN 139 257 NEUROTROPHIN-3.
FT DISULFID 152 217 BY SIMILARITY.
FT DISULFID 195 246 BY SIMILARITY.
FT DISULFID 205 248 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 257 AA; 29403 MW; EB537F85C5113B4 CRC64;

Query Match 36.9%; Score 468.5; DB 1; Length 257;
Best Local Similarity 39.7%; Pred. No. 3.8e-37;
Matches 102; Conservative 41; Mismatches 95; Indels 19; Gaps 5;

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1 MSILFTVMTFLVLYLNGIGDNNNDQSLPDSINSLITKLQADLLKKNKSKQVDTKRNQ 60
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46 TALRRASAPAAIAARVAGQTRNIT--VDPLRF--KRLRSFVLFSTQPPREADTQDL 103
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 STLPKAPRRPDEGGEPAKSFQPVYAMDTELLAQKRYKSPRYLSDSLPLPPPLYLM 120
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104 DFEVGAAPFSRTHRSKRSSSHPIFRGGEPSVCDVSVAWGDKTTATDICKKXENVLGEV 163
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121 EDVYGSFVAANRTRRRKRYAEHK--SHRGESVLCDSSESLVWTDKSAIDIRGHQVTVLGEI 179
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
164 NINNSVVKQYFFETKCRDPNPVDSGCGIGDSKHMNSYCTTHHTFYKALTMQ--GKQAAWRP 222
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Db	180	KSGNSPVKQYFETRECKEAPVYNGCRGIDDKHMNSOCTSOYVPAITSNNKLVGNRW	239
Qy	223	IRIDTACVCLSRKAVR	239
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Search completed: June 6, 2003, 10:49:55
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:49:38 ; Search time 17.5 Seconds

(without alignments)
1421.766 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268
Sequence: 1 MSMLPYTLITAFILGIGQAEF.....FIRIDTACCVLSRAAVRRA 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgm2_6/ptodata/2/pubpaa/US08_NEM_PUB pep.*
- 2: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/2/pubpaa/US06_NEM_PUB pep.*
- 4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgm2_6/ptodata/2/pubpaa/US07_NEM_PUB pep.*
- 6: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgm2_6/ptodata/2/pubpaa/PCTIS_PUBCOMB pep.*
- 8: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgm2_6/ptodata/2/pubpaa/US09_NEM_PUB pep.*
- 10: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgm2_6/ptodata/2/pubpaa/US10_NEM_PUB pep.*
- 12: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgm2_6/ptodata/2/pubpaa/US60_NEM_PUB pep.*
- 14: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	241	9	US-09-788-188-2
2	1265	99.8	241	8	US-08-450-842-5
3	1265	99.8	241	9	US-09-788-188-1
4	1265	99.8	241	9	US-10-150-262-3
5	1265	99.8	241	9	US-10-155-886-1
6	1265	99.8	241	9	US-10-155-886-6
7	1265	99.8	241	12	US-10-072-681-1
8	1261	99.4	241	10	US-09-822-263-16
9	1244	98.1	241	9	US-10-155-886-7
10	1102	86.9	241	9	US-10-155-886-8
11	1101	86.8	241	9	US-10-155-886-10
12	1091	86.0	241	9	US-10-155-886-9
13	783.5	61.8	243	9	US-10-155-886-11
14	768	60.6	235	9	US-10-155-886-12
15	651	51.3	120	9	US-10-155-886-13
16	651	51.3	120	9	US-10-155-886-14
17	648	51.1	121	12	US-10-072-681-2
18	648	51.1	157	10	US-09-798-338-4
19	647.5	51.1	167	10	US-09-798-338-8

20	642	50.6	153	10	US-09-798-338-2	Sequence 2, Appl1
21	642	50.6	163	10	US-09-798-338-6	Sequence 6, Appl1
22	621	49.0	121	9	US-09-813-398-9	Sequence 9, Appl1
23	614	48.4	121	9	US-10-155-886-33	Sequence 33, Appl1
24	602	47.5	120	9	US-10-155-886-35	Sequence 35, Appl1
25	584	46.1	118	9	US-10-155-886-40	Sequence 40, Appl1
26	584	46.1	120	9	US-10-155-886-38	Sequence 38, Appl1
27	584	46.1	121	12	US-10-072-681-3	Sequence 3, Appl1
28	566	44.6	117	9	US-10-155-886-42	Sequence 42, Appl1
29	507	40.0	121	9	US-10-155-886-37	Sequence 37, Appl1
30	500	39.4	125	9	US-10-155-886-35	Sequence 35, Appl1
31	479.5	37.8	257	9	US-09-788-188-6	Sequence 6, Appl1
32	476.5	37.6	257	8	US-08-450-842-4	Sequence 4, Appl1
33	476.5	37.6	257	9	US-09-788-188-5	Sequence 5, Appl1
34	476.5	37.6	257	9	US-10-155-886-3	Sequence 3, Appl1
35	469	37.0	260	9	US-10-155-886-20	Sequence 20, Appl1
36	467	36.8	258	9	US-10-155-886-18	Sequence 18, Appl1
37	466.5	36.8	257	9	US-10-155-886-19	Sequence 19, Appl1
38	466	36.8	258	9	US-10-155-886-17	Sequence 17, Appl1
39	452	35.6	142	8	US-08-450-842-52	Sequence 52, Appl1
40	390	30.8	72	10	US-09-848-664-21	Sequence 21, Appl1
41	388.5	30.6	119	10	US-09-745-032-6	Sequence 6, Appl1
42	388.5	30.6	119	10	US-09-742-600-6	Sequence 6, Appl1
43	388.5	30.6	119	10	US-09-872-090-6	Sequence 6, Appl1
44	388.5	30.6	120	10	US-09-745-032-3	Sequence 3, Appl1
45	388.5	30.6	120	10	US-09-742-600-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-788-188-2
; Sequence 2, Application US/09788188
; Publication No. US20030040082X1
; GENERAL INFORMATION:
; APPLICANT: TUESCH, MARK
; TITLE OF INVENTION: MUTANT PRO-NEUTROPHILIN WITH IMPROVED ACTIVITY
; FILE REFERENCE: 041673/2045
; CURRENT APPLICATION NUMBER: US/09/788, 188
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant NGF
; OTHER INFORMATION: pro-neutrophilin
US-09-788-188-2

Query Match	100.0%	Score 1268	DB 9	Length 241
Best Local Similarity	100.0%	Pred. No. 9.7e-124		
Matches 241	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSMLPYTLITAFILGIGQAEFHSSENYPAGHTIYQVMTKQHSLDLRLRRASAPAAIA	60	
DB	1	MSMLPYTLITAFILGIGQAEFHSSENYPAGHTIYQVMTKQHSLDLRLRRASAPAAIA	60	
QY	61	ARVAGOTRNTITVPRLFKKRLRSFVLSTOPRRAADODDFVGGAAPSRTRSK	120	
DB	61	ARVAGOTRNTITVPRLFKKRLRSFVLSTOPRRAADODDFVGGAAPSRTRSK	120	
QY	121	RSSSHPIFRGEFSVCDYSVWVGDTATIDIKGEWVILGEVNNINSYFKQYFFETKCR	180	
DB	121	RSSSHPIFRGEFSVCDYSVWVGDTATIDIKGEWVILGEVNNINSYFKQYFFETKCR	180	
QY	181	DPNPVDSGGRGIDSKRMNSYCTTHTFVVALTMDGQAMRFRIRITACCVLSRAAVR	240	
DB	181	DPNPVDSGGRGIDSKRMNSYCTTHTFVVALTMDGQAMRFRIRIDTACCVLSRAAVR	240	

QY 241 A 241
DB 241 A 241

RESULT 2

US-08-450-842-5
Sequence 5, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 23-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy B.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-450-842-5

Query Match 99.8%; Score 1265; DB 8; Length 241;
Best Local Similarity 99.6%; Pred. No. 2e-123;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
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QY 61 ARVAGOTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSTRHSK 120
DB 61 ARVAGOTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSTRHSK 120
QY 121 RSSHPIFHRGSEFVCDVSVMGDKTTATDIKGEVWVLGEVNNINSVFQYFFETKCR 180
DB 121 RSSHPIFHRGSEFVCDVSVMGDKTTATDIKGEVWVLGEVNNINSVFQYFFETKCR 180

QY 181 DPNVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAWFRIDTACVCLSRKAVR 240
DB 181 DPNVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAWFRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 3

US-09-788-188-1
Sequence 1, Application US/09788188
Publication No. US20030040082A1
GENERAL INFORMATION:
APPLICANT: TUSZYNSKI, MARK
APPLICANT: BLESCH, ARMIN
TITLE OF INVENTION: NOTANT PRO-NEUTROPHILIN WITH IMPROVED ACTIVITY
FILE REFERENCE: 041673/2045
CURRENT APPLICATION NUMBER: US/09/788,188
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-188-1

Query Match 99.8%; Score 1265; DB 9; Length 241;
Best Local Similarity 99.6%; Pred. No. 2e-123;
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QY 61 ARVAGOTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSTRHSK 120
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DB 121 RSSHPIFHRGSEFVCDVSVMGDKTTATDIKGEVWVLGEVNNINSVFQYFFETKCR 180
QY 181 DPNVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAWFRIDTACVCLSRKAVR 240
DB 181 DPNVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAWFRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-10-150-262-3
Sequence 3, Application US/10150262
Publication No. US20030049264A1
GENERAL INFORMATION:
APPLICANT: FOSTER, KEITH ALAN
APPLICANT: DUGGAN, MICHAEL JOHN
APPLICANT: SHONE, CLIFFORD CHARLES
TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
TITLE OF INVENTION: PERIPHERAL
TITLE OF INVENTION: SENSOR APPARENT FUNCTIONS
FILE REFERENCE: 023223/0104
CURRENT APPLICATION NUMBER: US/10/150,262
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/447,356
PRIOR FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 08/945,037
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: GB 9508204.6
PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 11
 / SOFTWAB: Patentin Ver. 2.1
 / SEQ ID NO 3
 / LENGTH: 241
 / TYPE: PRT
 / ORGANISM: Murine sp.
 US-10-150-262-3

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 DB 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 QY 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 QY 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240
 DB 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

US-10-155-886-1
 / Sequence 1, Application US/10155886
 / Publication No. US20030087804A1
 / GENERAL INFORMATION:
 / APPLICANT: Hemstead, Barbara L.
 / APPLICANT: Lee, Ramee
 / APPLICANT: Kermant, Pouneh
 / APPLICANT: Kermant, Pouneh
 / TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 / FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 / CURRENT APPLICATION NUMBER: US/10/155,886
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWAB: Patentin version 3.1
 / SEQ ID NO 1
 / LENGTH: 241
 / TYPE: PRT
 / ORGANISM: Homo sapien
 US-10-155-886-1

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 DB 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 QY 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 QY 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240
 DB 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240

QY 241 A 241
 DB 241 A 241

RESULT 6

US-10-155-886-6
 / Sequence 6, Application US/10155886
 / Publication No. US20030087804A1
 / GENERAL INFORMATION:
 / APPLICANT: Hemstead, Barbara L.
 / APPLICANT: Lee, Ramee
 / APPLICANT: Kermant, Pouneh
 / APPLICANT: Kermant, Pouneh
 / TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 / FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 / CURRENT APPLICATION NUMBER: US/10/155,886
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWAB: Patentin version 3.1
 / SEQ ID NO 6
 / LENGTH: 241
 / TYPE: PRT
 / ORGANISM: Homo sapien
 US-10-155-886-6

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHMTLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 DB 61 ARVAGQTRNITVDPLFKKRLRSRVLFPSTQPPREADTQDLDFEVGAAPFNRTHRSK 120
 QY 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFRGEFVSVCDSVWVGDKTTATDIDKKEVWVLGEVINNSVFKQYFETKCR 180
 QY 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240
 DB 181 DPNVDGCGRGIDSKHNSYCTTHTFPKALTMGKQAAAFIRIDTACVLSKAVAR 240
 QY 241 A 241
 DB 241 A 241

RESULT 7

US-10-072-681-1
 / Sequence 1, Application US/10072681
 / Patent No. US20020137893A1
 / GENERAL INFORMATION:
 / APPLICANT: Burton, Louis B.
 / APPLICANT: Schmelzer, Charles H.
 / TITLE OF INVENTION: PURIFICATION OF NGR
 / FILE REFERENCE: GENENT. 037C3
 / CURRENT APPLICATION NUMBER: US/10/072,681
 / CURRENT FILING DATE: 2002-02-08
 / PRIOR APPLICATION NUMBER: 60/030838
 / PRIOR FILING DATE: 1996-11-15
 / PRIOR APPLICATION NUMBER: 60/047855
 / PRIOR FILING DATE: 1997-05-29
 / PRIOR APPLICATION NUMBER: 08/970865
 / PRIOR FILING DATE: 1997-11-14
 / PRIOR APPLICATION NUMBER: 09/363573
 / PRIOR FILING DATE: 1999-07-29
 / PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-681-1

Query Match 99.8%; Score 1265; DB 12; Length 242;
Best Local Similarity 99.6%; Pred. No. 2e-123;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 2 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 61
QY 61 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 120
DB 62 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 121
QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 180
DB 122 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 181
QY 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 240
DB 182 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 241
QY 241 A 241
DB 242 A 242

RESULT 8

US-09-822-263-16
Sequence 16, Application US/09822263
Patent No. US20020036598A1

GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Vernet, Corine
APPLICANT: Shinkets, Richard A
APPLICANT: Burgess, Catherine
APPLICANT: Spytek, Kimberly
APPLICANT: Tchernyev, Velliar T
TITLE OF INVENTION: No. US20020036598A1 Polynucleotides and Polypeptides Encoded Th
FILE REFERENCE: 15966-572 CIP1
CURRENT APPLICATION NUMBER: US/09/822,263
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/672,665
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/156,745
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/158,942
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: 60/159,248
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/169,344
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/215,048
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-263-16

Query Match 99.4%; Score 1261; DB 10; Length 241;
Best Local Similarity 99.2%; Pred. No. 5.2e-123;
Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 120
DB 61 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 120
QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 180
DB 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 180
QY 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 240
DB 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 9

US-10-155-886-7
Sequence 7, Application US/10155886
Publication No. US20030087804A1

GENERAL INFORMATION:
APPLICANT: Hempstead, Barbara L.
APPLICANT: Lee, Ramee
APPLICANT: Teng, Kenneth K.
APPLICANT: Keramant, Pounch
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
CURRENT APPLICATION NUMBER: US/10/155,886
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 241
TYPE: PRT
ORGANISM: Gorilla gorilla
US-10-155-886-7

Query Match 98.1%; Score 1244; DB 9; Length 241;
Best Local Similarity 98.3%; Pred. No. 3e-121;
Matches 237; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTLLITAFILGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 120
DB 61 ARVAGQTRNITVDPRLPFKRRRLRSRPRVLFSTQPPREAADTODLDFEVGGAAPFSRTHRSK 120
QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 180
DB 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDIKKEVWVLGEVININNSVFQYFFETKCR 180
QY 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 240
DB 181 DNPVDSGCRGIDSKHNSYCTTHTTFVKALTMGKQAAWFRIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 10

US-10-155-886-8
Sequence 8, Application US/10155886
Publication No. US20030087804A1

GENERAL INFORMATION:
APPLICANT: Hempstead, Barbara L.

APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-155-886-8

Query Match 86.9%; Score 1102; DB 9; Length 241;
 Best Local Similarity 85.4%; Pred. No. 1,7e-106;
 Matches 205; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

1 MSMLFYTLITAFILGIGQAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIA 60
 1 MSMLFYTLITAFILGIGQAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIA 60
 61 ARVAGQTRNITVDPRFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSK 120
 61 ARVAGQTRNITVDPRFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSK 120
 121 RSSSHPIFRGSEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 121 RSSSHPIFRGSEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 121 RSTHVFHFMGEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 181 DNPVDSGGRGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240
 181 ARNPVDSGGRGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240

RESULT 11
 US-10-155-886-10
 Sequence 10, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 231
 TYPE: PRT
 ORGANISM: Bos taurus
 US-10-155-886-10

Query Match 86.8%; Score 1101; DB 9; Length 231;
 Best Local Similarity 90.3%; Pred. No. 2,1e-106;
 Matches 204; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

11 AFLIGIOAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIAARVAGQTRNI 70
 1 AFLIGIOAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIAARVAGQTRNI 70
 71 TVDPPLFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSKSSHPHIFR 130
 71 TVDPPLFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSKSSHPHIFR 130
 61 TVDPPLFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSKSSHPHIFR 120
 131 GEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCRDNPVDSGR 190
 131 GEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCRDNPVDSGR 190
 121 GEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCRDNPVDSGR 180

191 GIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSRK 236
 181 GIDAKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSRK 226

RESULT 12
 US-10-155-886-9
 Sequence 9, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 9
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-155-886-9

Query Match 86.0%; Score 1091; DB 9; Length 241;
 Best Local Similarity 84.6%; Pred. No. 2,4e-105;
 Matches 203; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

1 MSMLFYTLITAFILGIGQAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIA 60
 1 MSMLFYTLITAFILGIGQAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIA 60
 61 ARVAGQTRNITVDPRFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSK 120
 61 ARVAGQTRNITVDPRFKKRLRSRVLFTSTPPREAADTODLDFEYGAAPSRTRRSK 120
 121 RSSSHPIFRGSEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 121 RSSSHPIFRGSEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 121 RSTHVFHFMGEFVCDVSVMVGDKTTATDIDKGEVWVLGEVININNSVFKQYFFETKCR 180
 181 DNPVDSGGRGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240
 181 ASNPVDSGGRGIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240

RESULT 13
 US-10-155-886-11
 Sequence 11, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 11
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Gallus gallus
 US-10-155-886-11

Query Match 61.8%; Score 783.5; DB 9; Length 243;
 Best Local Similarity 64.5%; Pred. No. 2,2e-73;
 Matches 160; Conservative 21; Mismatches 48; Indels 19; Gaps 6;

1 MSMLFYTLITAFILGIGQAEHSESNVPAAGHTIPQVHWTQLQHSIDTLALRRASAPAAIA 56

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Db      5 MSMLYTLTLLIAFLITQAPKSEBNDGPLEYPAHSLPSTQNGQHI-----AKAAPQ 57
Qy      57 AAIARVA-----GGTRITVDPRLPKRRRLSPVLPTSTOPPREAATODLDEFGGA 111
Db      58 TTHGRFAMPDGTEDLNTAMDONTFKKRRSSSVLSTSTOPPSRKQSGTGF-LSSAV 115
Qy      112 PPSRTSRSSSHPIFHRGEFSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVK 171
Db      116 SLNRTARTGR-TAHPVLRGERSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVK 174
Qy      172 QYFETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 231
Db      175 QYFETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 234
Qy      232 VLSRAVR 239
Db      235 VLSRSGR 242

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RESULT 14

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US-10-155-886-12
; Sequence 12, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-155-886-12

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Query Match      60.6%; Score 768; DB 9; Length 235;
Best Local Similarity 63.2%; Pred. No. 8.6e-72;
Matches 153; Conservative 28; Mismatches 41; Indels 20; Gaps 6;

Qy      1 MSMLFYTLITAPLIGIAEPHSESNPAGHT---IP-QVHWTK-LQHSIDTLARRASA 54
Db      5 MSMLYTLTLLIAFLITQAPKSEBNDGPLEYPAHSLPSTQNGQHI-----AKAAPQ 57
Qy      55 PAAAIARVAGOTNTITVDPRLPKRRRLSPVLPTSTOPPREAATODLDEFGGAAPS 114
Db      54 -HGKLSAKRPSYFRNTVDPKLFKRRKSPVLFSTOPPLESDPQHLEY-LDDDESIN 111
Qy      115 RTRRSKSSSHPIFHRGEFSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVKOYE 174
Db      112 KITRAKR-TVHPVLRGERSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVKOYE 170
Qy      175 FETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLS 234
Db      171 FETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLS 230
Qy      235 RK 236
Db      231 RK 232

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RESULT 15

```

US-10-150-262-1
; Sequence 1, Application US/10150262
; Publication No. US20030049264A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, KEITH ALAN
; APPLICANT: DUGGAN, MICHAEL JOHN

```

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; APPLICANT: SHONE, CLIFFORD CHARLES
; TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
; TITLE OF INVENTION: PERIPHERAL
; TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS
; FILE REFERENCE: 023223/0104
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/10/150,262
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 08/945,037
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: GB 9508204.6
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-150-262-1

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```

Query Match      51.3%; Score 651; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      122 SSSHPHFHRGEFSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFRQYFETKCRD 161
Db      1 SSSHPHFHRGEFSVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFRQYFETKCRD 60
Qy      182 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLSRKAVRA 241
Db      61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLSRKAVRA 120

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Search completed: June 6, 2003, 10:52:46
 Job time : 17.5 secs

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OM protein - protein search, using SW model

Run on: June 6, 2003, 10:48:22 ; Search time 12.5 Seconds
(without alignment)
567.274 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268
Sequence: 1 MSMLFYLITAFILIGIOAEP.....FIRIDTACVCLSKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgml_6/prodata/1/1aa/5A COMB pep.*
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4: /cgml_6/prodata/1/1aa/6B COMB pep.*
5: /cgml_6/prodata/1/1aa/6C COMB pep.*
6: /cgml_6/prodata/1/1aa/backfile1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	99.8	241	1	US-08-266-080B-4
2	1265	99.8	241	1	US-08-451-947-5
3	1265	99.8	241	2	US-08-424-826A-5
4	1265	99.8	241	2	US-08-595-043A-75
5	1265	99.8	241	3	US-08-970-865-1
6	1265	99.8	241	3	US-08-928-694-5
7	1265	99.8	241	4	US-09-363-573-1
8	1265	99.8	241	4	US-09-447-356-3
9	1265	99.8	241	5	PCT-US91-06950-5
10	1265	99.8	241	5	PCT-US95-05423-4
11	1265	99.8	242	4	US-09-675-503-1
12	991	78.2	240	3	US-08-910-691-11
13	651	51.3	120	1	US-08-440-049-3
14	651	51.3	120	2	US-08-441-513A-3
15	651	51.3	120	3	US-08-841-663-31
16	651	51.3	120	4	US-08-845-541B-1
17	651	51.3	120	4	US-09-066-065A-1
18	651	51.3	120	4	US-09-447-356-1
19	651	51.3	120	4	US-09-664-295-31
20	651	51.3	120	5	PCT-US95-06918-3
21	648	51.1	120	3	US-08-970-865-2
22	648	51.1	120	4	US-09-363-573-2
23	648	51.1	121	4	US-09-675-503-2
24	648	51.1	157	4	US-09-675-922-4
25	647.5	51.1	167	4	US-09-675-922-8
26	642	50.6	119	3	US-08-753-642-2
27	642	50.6	153	4	US-09-675-922-2

28	642	50.6	163	4	US-09-675-922-6	Sequence 6, Appl1
29	637	50.2	120	4	US-08-845-541B-3	Sequence 3, Appl1
30	637	50.2	120	4	US-09-066-065A-3	Sequence 3, Appl1
31	634	50.0	120	4	US-08-845-541B-4	Sequence 4, Appl1
32	634	50.0	120	4	US-09-066-065A-4	Sequence 4, Appl1
33	629	49.6	120	4	US-08-845-541B-12	Sequence 12, Appl1
34	629	49.6	120	4	US-09-066-065A-12	Sequence 12, Appl1
35	628	49.5	120	4	US-08-845-541B-17	Sequence 17, Appl1
36	628	49.5	120	4	US-08-845-541B-20	Sequence 20, Appl1
37	628	49.5	120	4	US-09-066-065A-17	Sequence 17, Appl1
38	628	49.5	120	4	US-08-845-541B-20	Sequence 20, Appl1
39	626	49.4	120	4	US-08-845-541B-21	Sequence 21, Appl1
40	626	49.4	120	4	US-09-066-065A-18	Sequence 18, Appl1
41	626	49.4	120	4	US-09-066-065A-18	Sequence 18, Appl1
42	626	49.4	120	4	US-09-066-065A-21	Sequence 21, Appl1
43	623	49.1	120	4	US-08-845-541B-13	Sequence 13, Appl1
44	623	49.1	120	4	US-08-845-541B-19	Sequence 19, Appl1
45	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
TITLE OF INVENTION: Production of Biologically Active
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
US-08-266-080B-4

Query Match 99.8%; Score 1265; DB 1; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPLFKKRLRSRVL PSTOPPREADPTODLDFEVGGAAPFSTTRSK 120
DB 61 ARVAGOTRNTITVDPLFKKRLRSRVL PSTOPPREADPTODLDFEVGGAAPFSTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGCGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 2

US-08-451-947-5
Sequence 5, Application US/08451947
Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENE TECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451.947
FILING DATE:
CLASSIFICATION: 514
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2CID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-5

Query Match 99.8%; Score 1265; DB 1; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFTYLLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPLFKKRLRSRVL PSTOPPREADPTODLDFEVGGAAPFSTTRSK 120
DB 61 ARVAGOTRNTITVDPLFKKRLRSRVL PSTOPPREADPTODLDFEVGGAAPFSTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGCGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 3

US-08-424-826A-5
Sequence 5, Application US/08424826A
Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: Rosenthal, Arnon
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424.826A
FILING DATE: 19-APR-1995
CLASSIFICATION: 514
APPLICATION NUMBER: 08/240387
FILING DATE: 10-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-5

Query Match 99.8%; Score 1265; DB 2; Length 241;
Best Local Similarity 99.6%; Pred. No. 7,1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
DB 1 MSMLFYTLITFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
QY 61 ARVAGQTNITVDRLFKRRLRSRVLFTSTQPREADTDLDPEVGGAAPFSTTRSK 120
DB 61 ARVAGQTNITVDRLFKRRLRSRVLFTSTQPREADTDLDPEVGGAAPFSTTRSK 120
QY 121 RSSHPIFHGEFVCDVSVMVGDKTTATDIDKKEVMVLGEVINNSVFQYFFETKCR 180
DB 121 RSSHPIFHGEFVCDVSVMVGDKTTATDIDKKEVMVLGEVINNSVFQYFFETKCR 180
QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVFRIIDTACVLSKAVRR 240
DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVFRIIDTACVLSKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-08-595-043A-75
Sequence 75, Application US/08595043A
Patent No. 593824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-75

Query Match 99.8%; Score 1265; DB 2; Length 241;
Best Local Similarity 99.6%; Pred. No. 7,1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
DB 1 MSMLFYTLITFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSIDTALRRASAPAAIA 60
QY 61 ARVAGQTNITVDRLFKRRLRSRVLFTSTQPREADTDLDPEVGGAAPFSTTRSK 120
DB 61 ARVAGQTNITVDRLFKRRLRSRVLFTSTQPREADTDLDPEVGGAAPFSTTRSK 120
QY 121 RSSHPIFHGEFVCDVSVMVGDKTTATDIDKKEVMVLGEVINNSVFQYFFETKCR 180
DB 121 RSSHPIFHGEFVCDVSVMVGDKTTATDIDKKEVMVLGEVINNSVFQYFFETKCR 180
QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVFRIIDTACVLSKAVRR 240
DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVFRIIDTACVLSKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 5

US-08-970-865-1
Sequence 1, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94060
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
CLASSIFICATION: 530
APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-970-865-1

Query Match 99.8%; Score 1265; DB 3; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOABPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFYTLITAFILGIOABPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGOTRNTITVDPPLFKKRLRSRVLFTSTOPPREAADTODLDFEVGAAPFSRTHSK 120
DB 61 ARVAGOTRNTITVDPPLFKKRLRSRVLFTSTOPPREAADTODLDFEVGAAPFSRTHSK 120
QY 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 6

US-08-928-694-5
Sequence 5, Application US/08928694
Patent No. 6037320

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-Sep-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION: P0666P2C1D2C1

TELEPHONE:

TELEFAX: 650/952-9881

TELEFAX:

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-928-694-5

Query Match 99.8%; Score 1265; DB 3; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOABPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFYTLITAFILGIOABPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGOTRNTITVDPPLFKKRLRSRVLFTSTOPPREAADTODLDFEVGAAPFSRTHSK 120
DB 61 ARVAGOTRNTITVDPPLFKKRLRSRVLFTSTOPPREAADTODLDFEVGAAPFSRTHSK 120
QY 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 7

US-09-363-573-1
Sequence 1, Application US/09363573
Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,573

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/970,865

FILING DATE: 5/29/1997

APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/047855

FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: P1063R2

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-363-573-1

Query Match 99.8%; Score 1265; DB 4; Length 241;
 Best Local Similarity 99.6%; Pred. No. 7.1e-142;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 QY 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 8

US-09-447-356-3
 Sequence 3, Application US/09447356
 Patent No. 639513

GENERAL INFORMATION:
 APPLICANT: POSTER, KEITH ALAN
 APPLICANT: DUGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIUM TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
 TITLE OF INVENTION: SENSOR APPARENT FUNCTIONS
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/09/447,356
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-09-447-356-3

Query Match 99.8%; Score 1265; DB 4; Length 241;
 Best Local Similarity 99.6%; Pred. No. 7.1e-142;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 QY 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240

DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9

PCT-US91-06950-5

Sequence 5, Application PC/TUS9106950
 GENERAL INFORMATION:

APPLICANT: GENE TECH, INC.
 APPLICANT: ROSENTHAL, ARNON
 TITLE OF INVENTION: NOVEL NEUTROTROPIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06950
 FILING DATE: 19910924
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 ATTORNEY/AGENT INFORMATION:
 NAME: Hensley, Max D.
 REGISTRATION NUMBER: 27,043
 REFERENCE/DOCKET NUMBER: 666P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-06950-5

Query Match 99.8%; Score 1265; DB 5; Length 241;
 Best Local Similarity 99.6%; Pred. No. 7.1e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLITLAFILGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTHSK 120
 QY 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRGSEFVCDVSVMVGDKTATDIDKGEVWVLGSEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAWRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10

PCT-US95-05423-4
 Sequence 4, Application PC/TUS9505423
 GENERAL INFORMATION:
 APPLICANT: Jack Lile
 APPLICANT: Tadahiko Kohno
 APPLICANT: Duane Bonam
 APPLICANT: Mary S. Rosendahl
 TITLE OF INVENTION: Production of Biologically Active
 TITLE OF INVENTION: Recombinant Neurotrophic Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Bratschun, L.L.C.
 STREET: 8400 E. Prentice Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05423
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/266,090
 FILING DATE: 27-JUNE-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/240,122
 FILING DATE: 09-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/087,912
 FILING DATE: 06-JULY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/680,681
 FILING DATE: 04-APRIL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/594,126
 FILING DATE: 09-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/547,750
 FILING DATE: 02-JULY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/505,441
 FILING DATE: 06-APRIL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: SYNE200/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: inferred amino acid sequence of human NGF
 PCT-US95-05423-4

Query Match 99.8%; Score 1265; DB 5; Length 241;
 Best Local Similarity 99.6%; Pred. No. 7,1e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60
 DB 1 MSMLFTLLTAFLIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60

QY 61 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTQPREADTDODLFEVGAAPESRTRSK 120
 DB 61 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTQPREADTDODLFEVGAAPFNRTRSK 120
 QY 121 RSSHPPIFRGSEFVCDVSVMVGDKTATDIDKEVWVGEVINNSVFOYFEETKCR 180
 DB 121 RSSHPPIFRGSEFVCDVSVMVGDKTATDIDKEVWVGEVINNSVFOYFEETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAAVFRIDTACVLSRAVVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAAVFRIDTACVLSRAVVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 11

US-09-675-503-1
 Sequence 1, Application US/09675503
 Patent No. 6423831
 GENERAL INFORMATION:
 APPLICANT: Burton, Louis E.
 APPLICANT: Schmelzer, Charles H.
 APPLICANT: Beck, Joanne T.
 TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
 TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
 FILE REFERENCE: GENE 037C2
 CURRENT APPLICATION NUMBER: US/09/675,503
 CURRENT FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/030838
 PRIOR FILING DATE: 1996-11-15
 PRIOR APPLICATION NUMBER: 60/047855
 PRIOR FILING DATE: 1997-05-29
 PRIOR APPLICATION NUMBER: 08/970865
 PRIOR FILING DATE: 1997-11-14
 PRIOR APPLICATION NUMBER: 09/363573
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-675-503-1

Query Match 99.8%; Score 1265; DB 4; Length 242;
 Best Local Similarity 99.6%; Pred. No. 7,2e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60
 DB 2 MSMLFTLLTAFLIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 61
 QY 61 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTQPREADTDODLFEVGAAPESRTRSK 120
 DB 62 ARVAGOTRNITVDPRLFKKRLRSRVLFTSTQPREADTDODLFEVGAAPFNRTRSK 121
 QY 121 RSSHPPIFRGSEFVCDVSVMVGDKTATDIDKEVWVGEVINNSVFOYFEETKCR 180
 DB 122 RSSHPPIFRGSEFVCDVSVMVGDKTATDIDKEVWVGEVINNSVFOYFEETKCR 181
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAAVFRIDTACVLSRAVVR 240
 DB 182 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMDGKQAAVFRIDTACVLSRAVVR 241
 QY 241 A 241
 DB 242 A 242

RESULT 12

US-08-910-691-11

/ Sequence 11, Application US/08910691
/ Patent No. 6015552

/ GENERAL INFORMATION:

/ APPLICANT: MATANABE, Tatsuya

/ APPLICANT: YOSHITOMI, Sumie

/ TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA

/ NUMBER OF SEQUENCES: 12

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

/ STREET: 130 Water Street

/ CITY: Boston

/ STATE: Massachusetts

/ COUNTRY: US

/ ZIP: 02109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/910,691

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/074,969

/ FILING DATE: 19930604

/ ATTORNEY/AGENT INFORMATION:

/ NAME: NEUMER, George W

/ REGISTRATION NUMBER: 26964

/ REFERENCE/DOCKET NUMBER: 12345

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (617) 523-3400

/ TELEFAX: (617) 523-6440

/ TELETYPE: 200291 STRS UR

/ INFORMATION FOR SEQ ID NO: 11:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 240 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

US-08-910-691-11

Query Match Best Local Similarity 78.8%; Score 991; DB 3; Length 240;

Matches 189; Conservative 20; Mismatches 29; Indels 2; Gaps 2;

QY 1 MSMLFYLLITFLIGIQAPHSSESNVPAGHTIPGVHTKLOHSIDTALRRASPAALIA 60

DB 1 MSMLFYLLITFLIGIQAPHSSESNVPAGHTIPGVHTKLOHSIDTALRRASPAALIA 60

QY 61 ARVAGQTRNITVDPRLEPKRRRLSPRVLFSTQPREADTODLPEVGAAPFRTTRSK 120

DB 61 ARVAGQTRNITVDPRLEPKRRRLSPRVLFSTQPREADTODLPEVGAAPFRTTRSK 120

QY 121 RSSHPIFRHGESEVSVVWGDKTATDIKKEVAVLGEVINNSVFPQYFEETKCR 180

DB 121 RYAEHR-SHGESESVCSSESLMTDKSALDIRHQVTVLGEITGNSPVQYFEETRCK 179

QY 181 DPNPVDGCRGIDSKHNSYCTTHTFVKALTMQD-KQOAMRFIRIDTACVCLSRKAVR 239

DB 180 EAPFVKRGCGIDSKHNSYCTTHTFVKALTMQD-KQOAMRFIRIDTACVCLSRKAVR 239

RESULT 13

US-08-440-049-3

/ Sequence 3, Application US/08440049

/ Patent No. 5728803

/ GENERAL INFORMATION:

/ APPLICANT: Ulfert, Roman

/ APPLICANT: Presta, Leonard G.

/ APPLICANT: Winslow, John W.

/ TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS

/ NUMBER OF SEQUENCES: 7

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Genentech, Inc.

/ STREET: 460 Point San Bruno Blvd

/ CITY: South San Francisco

/ STATE: California

/ COUNTRY: USA

/ ZIP: 94080

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

/ OPERATING SYSTEM: IBM PC compatible

/ SOFTWARE: Winpatin (Genentech)

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/440,049

/ FILING DATE: 12-May-1995

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/253937

/ FILING DATE: 03-JUN-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Torchia, Timothy R.

/ REGISTRATION NUMBER: 36,700

/ REFERENCE/DOCKET NUMBER: P0905C2

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 415/225-8674

/ TELEFAX: 415/952-9861

/ TELETYPE: 910/371-7168

/ INFORMATION FOR SEQ ID NO: 3:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 120 amino acids

/ TYPE: Amino Acid

/ TOPOLOGY: Linear

US-08-440-049-3

Query Match Best Local Similarity 51.3%; Score 651; DB 1; Length 120;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPFRHGESEVSVVWGDKTATDIKKEVAVLGEVINNSVFPQYFEETKCRD 181

DB 1 SSSHPFRHGESEVSVVWGDKTATDIKKEVAVLGEVINNSVFPQYFEETKCRD 60

QY 182 DPNPVDGCRGIDSKHNSYCTTHTFVKALTMQD-KQOAMRFIRIDTACVCLSRKAVR 241

DB 61 DPNPVDGCRGIDSKHNSYCTTHTFVKALTMQD-KQOAMRFIRIDTACVCLSRKAVR 120

RESULT 14

US-08-441-513A-3

/ Sequence 3, Application US/08441513A

/ Patent No. 5961480

/ GENERAL INFORMATION:

/ APPLICANT: Ulfert, Roman

/ APPLICANT: Presta, Leonard G.

/ TITLE OF INVENTION: Pantropic Neurotrophic Factors

/ NUMBER OF SEQUENCES: 20

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Genentech, Inc.

/ STREET: 1 DNA Way

/ CITY: South San Francisco

/ STATE: California

/ COUNTRY: USA

/ ZIP: 94080

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

/ OPERATING SYSTEM: IBM PC compatible

/ SOFTWARE: Winpatin (Genentech)

/ CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-3

Query Match 51.3%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPFHRGERSVCDVSVMVGDKTATDINGKKEVMVLGEVNNINSVFKQYFFETKCRD 181
DB 1 SSSHPFHRGERSVCDVSVMVGDKTATDINGKKEVMVLGEVNNINSVFKQYFFETKCRD 60
QY 182 PNPVDSGCGIDSKHMNSYCTTHTFYKALTMDSKQAAWRFIRIDTACVCLSRKAVRA 241
DB 61 PNPVDSGCGIDSKHMNSYCTTHTFYKALTMDSKQAAWRFIRIDTACVCLSRKAVRA 120

RESULT 15
US-08-581-662-31

/ Sequence 31, Application US/08581662
/ Patent No. 6121235
/ GENERAL INFORMATION:
/ APPLICANT: Gao, Wei-Qiang
/ TITLE OF INVENTION: Treatment of Balance Impairments
/ FILE REFERENCE: P0981
/ CURRENT APPLICATION NUMBER: US/08/581,662
/ NUMBER OF SEQ ID NOS: 36
/ SEQ ID NO 31
/ LENGTH: 120
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-08-581-662-31

Query Match 51.3%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPFHRGERSVCDVSVMVGDKTATDINGKKEVMVLGEVNNINSVFKQYFFETKCRD 181
DB 1 SSSHPFHRGERSVCDVSVMVGDKTATDINGKKEVMVLGEVNNINSVFKQYFFETKCRD 60
QY 182 PNPVDSGCGIDSKHMNSYCTTHTFYKALTMDSKQAAWRFIRIDTACVCLSRKAVRA 241
DB 61 PNPVDSGCGIDSKHMNSYCTTHTFYKALTMDSKQAAWRFIRIDTACVCLSRKAVRA 120

Search completed: June 6, 2003, 10:52:05
Job time: 13.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 10:46:22 ; Search time 32.5 Seconds
(without alignments)
988.105 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268
Sequence: 1 MSMLFYLITLAFILGIAQAP.....FIRIDTACVTLSHKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneeq/geneeq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneeq/geneeq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneeq/geneeq-emb1/AA1982.DAT.*
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21: /SID52/gcgdata/geneeq/geneeq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneeq/geneeq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneeq/geneeq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	99.8	241	AA13063	Human NGF Smat-Apa
2	1265	99.8	241	AA11474	Human nerve growth
3	1265	99.8	241	AA13858	Human nerve growth
4	1265	99.8	241	AA17419	Human nerve growth
5	1265	99.8	241	AA16688	Human nerve growth
6	1265	99.8	241	AA26237	Human preproNGF
7	1265	99.8	241	AA48886	Human prepro-nerve
8	1265	99.8	241	AA107303	Human nerve growth
9	1265	99.8	241	AA166929	Human NGF. Homo s
10	1265	99.8	241	AA18904	Human beta nerve g

11	1265	99.8	241	23	AB04994	Human beta nerve g
12	1265	99.8	245	5	AA14038	Sequence encoded b
13	1262	99.5	307	14	AA15241	Human pre-pro nerv
14	1261	99.4	241	22	AA16785	Amino acid sequenc
15	1261	99.4	307	14	AA13799	Human NGF. Homo s
16	1259	99.3	307	19	AA169725	Human beta-nerve g
17	1233	97.2	239	14	AA143910	Nerve growth facto
18	1183.5	93.3	241	12	AA13886	NGF with pro-regio
19	1170	92.3	222	21	AA10884	Human proNGF prote
20	1091	86.0	240	23	AA150845	Mouse nerve growth
21	1091	86.0	307	5	AA140036	Sequence encoded b
22	1091	86.0	307	5	AA140039	Sequence encoded b
23	1088	85.8	307	14	AA145240	Cloned mouse pre-p
24	991	78.2	240	15	AA156451	Sequence of pro re
25	991	77.8	240	15	AA156451	Human NGF-2/NT-3 e
26	986	77.8	240	13	AA126273	NGF/NT-3 in PTB13
27	682	53.8	129	14	AA137539	Recombinant beta-N
28	682	53.8	129	18	AA124145	Recombinant mini-f
29	661	52.1	124	13	AA121851	Chimeric neurotrop
30	657.5	51.9	154	13	AA122751	Human growth hormo
31	651	51.3	120	20	AA181117	Nerve growth facto
32	651	51.3	120	21	AA129141	N-terminal of neut
33	651	51.3	120	22	AA164994	Nerve growth facto
34	651	51.3	120	22	AA135944	NGF-beta amino aci
35	648	51.1	156	23	AA150303	Nerve growth facto
36	648	51.1	157	21	AA101596	Nerve growth facto
37	648	51.1	157	22	AA167677	Amino acid sequenc
38	648	51.1	157	23	AA108525	Synthetic nerve gr
39	647.5	51.1	166	23	AA150301	Nerve growth facto
40	647.5	51.1	167	22	AA167679	Nerve growth facto
41	647	51.0	261	10	AA191299	Amino acid sequenc
42	647	51.0	262	7	AA151033	Human nerve growth
43	643	50.7	120	17	AA190531	Human beta-nerve g
44	642	50.6	118	10	AA191034	Paritropic neurotro
45	642	50.6	119	5	AA140040	Human nerve growth

ALIGNMENTS

RESULT 1	AA13063	AA13063 standard; Protein; 241 AA.
ID	AA13063	
AC	AA13063	
XX		
DT	30-SEP-1991 (first entry)	
XX		
DE	Human NGF Smat-Apai fragment prod.	
XX		
KW	Expression vector; human nerve growth factor; yeast;	
KM	benile dementia.	
XX		
OS	Homo sapiens.	
XX		
PN	JP03139285-A.	
XX		
PD	13-JUN-1991.	
XX		
PF	20-DEC-1989; 89JP-0328199.	
XX		
PR	27-JUL-1989; 89JP-0192581.	
XX		
PA	(TAKE) TAKEDA CHEMICAL IND KK.	
XX		
DR	WPI: 1991-218449/30.	
XX		
DR	N-PSDB; AAQ12638.	
XX		
PT	New yeast expression vector - used in prodn. of human nerve growth	
XX		
XX	factor from corresp. yeast.	
PS	Disclosure; Fig 1(1-2); 14pp; Japanese.	
XX		

CC Human NGF is useful as a reagent for study of the nervous system, and
 CC for treatment of senile dementia. The DNA encoding this fragment was
 CC derived from the human gene or is synthesised chemically.
 CC See also AAQ12639.
 XX
 SQ Sequence 241 AA;

Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFTLLTAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREAADTODLDFEVGAAPFSTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREAADTODLDFEVGAAPFSTRSK 120
 QY 121 RSSSHPIFHRGEPFVCDVSVMWGDXTATDINGKKEVMVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGEPFVCDVSVMWGDXTATDINGKKEVMVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSRKAVRR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 2
 AAR11474
 ID AAR11474 standard; Protein; 241 AA.

AC AAR11474;
 DT 26-APR-1991 (first entry)
 DE Human nerve growth factor.
 KW NGF; senile dementia.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..18
 FT Protein /label= signal sequence
 FT Protein 19..241
 FT Protein /label= pro-NGF
 FT Protein 122..241
 FT Disulfide-bond /label= mature NGF
 FT Disulfide-bond 135..202
 FT Disulfide-bond 180..230
 FT Disulfide-bond 190..232
 XX
 XX EP41451-A.
 XX
 XX 27-FEB-1991.
 XX
 XX 17-AUG-1990; 90EP-0115815.
 XX
 XX 21-AUG-1989; 89JP-0212980.
 XX 20-DEC-1989; 89JP-0328198.
 XX 13-APR-1990; 90JP-0096252.
 XX 07-JUN-1990; 90JP-0147392.
 XX
 XX (TAKE) TAKEDA CHEMICALS IND KK.
 XX Kakinuma A, Nakahama K, Yoshimura K, Katsubo Y, Iwano M,
 XX WPI, 1991-059398/09.

DR N-PSDB; AAQ10620.
 XX
 XX Human nerve growth factor containing cysteine residues - used as
 PT reagent and therapeutic drug for senile dementia.
 XX
 PS Claim 1; Fig 1; 33pp; English.

The sequence was deduced from a clone isolated from a lambda EMBL3
 CC genomic library prepd. from human leukocyte DNA, using a probe [A.
 CC synthesised based on the sequence of the known human NGF gene [A.
 CC Ullrich et al., Nature 303, 821 (1983)]. The clone, betaLN2113,
 CC isolated from the library was cleaved with SmaI and ApaI to remove
 CC a 1kb fragment contg. the gene which was then inserted into plasmid
 CC pBlueScript IIX to obtain pNGFP107G. The gene was sequenced from
 CC this plasmid using SeeDease (Biochemical). The sequence of the
 CC protein coding region was found to be in complete agreement with
 CC that of Ullrich et al. The sequence was used to produce
 CC recombinant h-NGF for use in the prodn. of drugs for e.g. senile
 CC dementia.

Sequence 241 AA;

Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFTLLTAFILGIGQAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREAADTODLDFEVGAAPFSTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREAADTODLDFEVGAAPFSTRSK 120
 QY 121 RSSSHPIFHRGEPFVCDVSVMWGDXTATDINGKKEVMVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGEPFVCDVSVMWGDXTATDINGKKEVMVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSRKAVRR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAAFRIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 3
 AAR13858
 ID AAR13858 standard; Protein; 241 AA.

AC AAR13858;
 DT 21-NOV-1991 (first entry)
 DE Human nerve growth factor.
 KW hNGF.
 OS Homo sapiens.
 XX
 XX 31-UTL-1991.
 XX
 XX 12-DEC-1989; 89JP-0320483.
 XX
 XX 30-SEP-1989; 89JP-0253796.
 XX 15-DEC-1989; 89JP-0314860.
 XX 12-DEC-1989; 89JP-0320483.
 XX
 XX (TAKE) TAKEDA CHEMICAL IND KK.

DR WPI: 1991-269694/37.
 DR N-PSDB; AAQ13397.
 XX
 PT Secretory prepn. of animal protein - by culturing
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of
 PT promoter region.
 XX
 PS Disclosure; Fig 3; 12pp; Japanese.
 CC
 CC The amino acid sequence is encoded that of human nerve growth factor
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the
 CC glyceraldehyde-3-phosphate dehydrogenase (GHD) gene promoter.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFLLGLOAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFLLGLOAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQRTNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 DB 61 ARVAGQRTNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 QY 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240
 DB 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 Db
 QY 241 A 241
 Db
 RESULT 4
 AAR77419 standard; Protein; 241 AA.
 XX ID AAR77419;
 XX AC AAR77419;
 XX DT 10-FEB-1996 (first entry)
 XX DE Human nerve growth factor.
 XX KW Nerve growth factor; neurotrophic factor; therapeutic;
 XX KW protein refolding; NGF.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 122..241
 FT /note= "mature protein"
 FT Region 1..121
 FT /note= "pre-region"
 XX
 PN MO9530686-A1.
 XX
 PD 16-NOV-1995.
 XX
 PF 02-MAY-1995; 95MO-US05423.
 XX
 PR 27-JUN-1994; 94US-0266080.
 XX
 PR 09-MAY-1994; 94US-0240122.
 XX
 PA (SYNT) SYNTEX-SYNERGEN NEUROSCIENCE JOINT VENTU.
 XX
 PI Bonam D, Kohno T, Lile J, Rosendahl MS;

XX
 DR WPI: 1995-404080/51.
 DR N-PSDB; AAT05437.
 XX
 PT Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.
 XX
 PS Disclosure; Page 33-34; 57pp; English.
 CC
 CC The nerve growth factor (NGF) gene is expressed in *Bacterichia*
 CC coli cells. The recombinant protein is solubilized and
 CC sulfonlated and allowed to refold in the presence of PEG and urea.
 CC Biologically active NGF, used for promoting the survival of and
 CC maintaining the phenotypic differentiation of nerve and glial cells,
 CC is isolated and purified. This method breaks incorrectly formed
 CC disulfide bonds and allows refolding of the factor into the correct
 CC tertiary structure required for maximum yield of full active protein.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 16; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFLLGLOAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFLLGLOAEPSHSNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQRTNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 DB 61 ARVAGQRTNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 QY 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVNLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240
 DB 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 Db
 QY 241 A 241
 Db
 RESULT 5
 AAR66688 standard; Protein; 241 AA.
 XX ID AAR66688;
 XX AC AAR66688;
 XX DT 23-AUG-1995 (first entry)
 XX DE Human nerve growth factor.
 XX KW Human nerve growth factor; hNGF; polyclonal antibody;
 XX KW immunogen; enzyme immunoassay.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= sig_peptide
 FT Peptide 19..121
 FT /label= pro_peptide
 FT Misc-difference 8
 FT /note= "corresponding codon TCG"
 FT Misc-difference 59
 FT /note= "corresponding codon TAT"
 FT Misc-difference 173
 FT /note= "corresponding codon TAG"
 FT Disulfide-bond 136..201

FT Disulfide-bond 179..229
XX Disulfide-bond 189..231
XX JF06317587-A.
XX
XX 15-NOV-1994.
XX
XX 14-FEB-1991; 91JP-0021181.
XX
XX 31-AUG-1990; 90JP-0231317.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI; 1995-033116/05.
XX N-PSDB; AAQ79871.
XX
XX Polyclonal antibody against human nerve growth factor (NGF) -
XX useful to detect human NGF, for diagnosis of disease
XX
XX Example 1; Pages 31-33; 35pp; Japanese.
XX
XX AAQ79871 encodes AAR6688 human nerve growth factor (hNGF), the
XX protein was used as an immunogen to generate a polyclonal
XX antibody against hNGF. The polyclonal antibody can be used
XX to detect and determine hNGF pref. by enzyme immunoassay.
XX
SQ Sequence 241 AA;
Query Match 99.8%; Score 1265; DB 16; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTQPPREADTDLDPEVGGAAPFRTTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTQPPREADTDLDPEVGGAAPFRTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMWGDXTATDIDIKGEVMVLGEVINNSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMWGDXTATDIDIKGEVMVLGEVINNSVFQYFEETKCR 180
QY 181 DPNPVDSCGKIDSKMNSYCTTHTFVKALTMDGKQAAWRFIRIDTACVLSRKAVRR 240
DB 181 DPNPVDSCGKIDSKMNSYCTTHTFVKALTMDGKQAAWRFIRIDTACVLSRKAVRR 240
QY 241 A 241
DB 241 A 241
RESULT 6
ID AAW26237 standard; Protein; 241 AA.
XX AAW26237;
XX
XX 16-MAR-1998 (first entry)
XX
XX Human preproNGF.
XX
XX Fusion protein; hydrophilic spacer; recombinant; expression system;
XX carboxypeptidase; preproNGF.
XX
XX Homo sapiens.
XX
XX W09728272-A1.
XX
XX 07-AUG-1997.
XX
XX 31-JAN-1997; 97WO-US01470.

XX
XX 31-JAN-1996; 96US-0595043.
XX
XX (TECH-) TECHNOLOGENE INC.
XX
XX Sgarlato GD;
XX
XX WPI; 1997-402624/37.
XX
XX N-PSDB; AAT80162.
XX
XX Recombinant protein expression system for fusion protein production
XX - useful for high quantity production of authentic recombinant
XX proteins
XX
XX Example 6; Page 140-141; 194pp; English.
XX
XX A novel recombinant vector has been developed which comprises a
XX nucleotide sequence encoding a fusion protein. The fusion protein
XX comprises three domains joined together in order, from N-terminus to
XX C-terminus, of a first domain comprising a protein of interest, a second
XX domain comprising a hydrophilic spacer and an affinity domain, each
XX domain comprising amino acid residues. The present sequence represents
XX human preproNGF, used in example 6 of the present invention. The
XX recombinant vector is used for the production of authentic recombinant
XX proteins of interest. The method of the invention is useful for the
XX expression of fusion proteins capable of isolation by affinity
XX chromatography in pro- or eukaryotic cells. This method allows
XX for the efficient cleavage and generation of authentic proteins of
XX interest that do not contain extraneous (i.e. non-naturally occurring)
XX amino acids.
XX
SQ Sequence 241 AA;
Query Match 99.8%; Score 1265; DB 18; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTQPPREADTDLDPEVGGAAPFRTTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSRVLFTSTQPPREADTDLDPEVGGAAPFRTTRSK 120
QY 121 RSSSHPIFRHGEFSVCDVSVMWGDXTATDIDIKGEVMVLGEVINNSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMWGDXTATDIDIKGEVMVLGEVINNSVFQYFEETKCR 180
QY 181 DPNPVDSCGKIDSKMNSYCTTHTFVKALTMDGKQAAWRFIRIDTACVLSRKAVRR 240
DB 181 DPNPVDSCGKIDSKMNSYCTTHTFVKALTMDGKQAAWRFIRIDTACVLSRKAVRR 240
QY 241 A 241
DB 241 A 241
RESULT 7
ID AAW48886 standard; Protein; 241 AA.
XX AAW48886;
XX
XX 12-OCT-1998 (first entry)
XX
XX Human prepro-nerve growth factor beta chain.
XX
XX Neurotrophin; nerve growth factor; NGF; human; purification;
XX hydrophobic interaction chromatography.
XX
XX Homo sapiens.
XX
XX

PH	Key	Location/Qualifiers
PT	Protein	1..121
PT	Protein	/label= Prepro_region
PT	Protein	122..241
PT	Modified-site	/label= Mat_protein
PT	Region	167
PT	Region	/note= "N-glycosylated"
PT	Region	179..189
PT	Region	/note= "conserved Cys-containing region involved in Cys knot motif"
PT	Region	229..231
PT	Region	/note= "conserved Cys-containing region involved in Cys knot motif"
PN	WO9821234-A2.	
PD	22-MAY-1998.	
PD	14-NOV-1997;	97WO-US21068.
PR	29-MAY-1997;	97US-0047855.
PR	15-NOV-1996;	96US-0030838.
PA	(GETH) GENENTECH INC.	
PI	Beck JT, Burton LE, Schmelzer CH;	
DR	WPI, 1998-322333/28.	
XX	Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated variant(s) - using hydrophobic interaction chromatography, optionally in combination with high performance cation exchange chromatography	
XX	Disclosure; Fig 4; 59pp; English.	
XX	This polypeptide comprises the human nerve growth factor (NGF) beta chain precursor. Methods are provided for large-scale purification of neurotrophins, including mature NGF, suitable for clinical use. A claimed method comprises: (1) separating the neurotrophin from the other proteins using a hydrophobic interaction chromatography resin (HIC); and optionally (2) separating the neurotrophin from a chemical variant by high performance cation exchange chromatography (HPEC). The processes can also be used for purification of e.g. mouse NGF (see AAM48867), brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow separation of neurotrophins from various undesirable misprocessed, misfolded, site, glycosylated or charge forms. They allow selective separation from their variants and other molecules, and from other polypeptides with high pl. The processes are applicable to starting materials from various sources, including fermentation broths or lysed bacterial or mammalian cells.	
XX	Sequence 241 AA;	
XX	Query Match 99.8%; Score 1365; DB 19; Length 241; Best Local Similarity 99.6%; Pred. No. 1.6e-133; Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
QY	1 MSMLFYTLITFLGLIOAEPHSESVAPGHTIPQVHWTKLQHSIDLTALRRASAPAAIA 60	
QY	1 MSMLFYTLITFLGLIOAEPHSESVAPGHTIPQVHWTKLQHSIDLTALRRASAPAAIA 60	
QY	61 ARVAGQENITVDPRLPFCKRLRSPLVFSSTQPREADTDLDPEVGGAAPFSRTHSK 120	
QY	61 ARVAGQENITVDPRLPFCKRLRSPLVFSSTQPREADTDLDPEVGGAAPFSRTHSK 120	
QY	121 RSSSHPIPIHREGEFSVCDVSVMVGDKTATATIKGKEVWVLGEVINNSVFPQYFEETKCR 180	
QY	121 RSSSHPIPIHREGEFSVCDVSVMVGDKTATATIKGKEVWVLGEVINNSVFPQYFEETKCR 180	
QY	181 DPNVDSGCRGIDSKHNSYCTTHTHTFKALITMDGKAAMFIRIDTACVLSRAVRR 240	

Dd		181 DPPPVSGCGRGIDSKMNSYCTTHTFVALLTMGQAAAFRIIDPACVCVSRAVR	240
Oy	241 A 241 241 A 241		
ID	AAY07303 standard; Protein; 241 AA.		
XX AC	AAY07303;		
DT XX	06-JUL-1999 (first entry)		
DE XX	Human nerve growth factor beta protein.		
KW KM	Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF2; expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3; NT3; voluntary motor function.		
XN OS	Homo sapiens.		
PX PN	M09900148-A2.		
PD PD	07-JAN-1999.		
PF PF	30-JUN-1998; 98MO-USL3778.		
PR PR	30-JUN-1997; 97US-0051255. (REGC) UNIV CALIFORNIA.		
PI PI	Gage FH, Grill R, Tuszynski MH; MPI: 1999-095478/08. N-PDSB; AAX34366.		
PT PT	Treating spinal cord injuries in a mammal - by inducing growth of cerebrospinal projection axons using a recombinant vector for expressing CST neurotrophin		
PS PS	Disclosure; Fig 6; 49pp; English.		
CC CC	The invention relates to a method of inducing cerebrospinal projection (CST) axon growth in a mammal with a spinal cord injury that involves a CST lesion by delivering a recombinant expression vector for CST neurotrophin, such as this sequence - nerve growth factor beta. The method is used to induce partial recovery of voluntary motor function in a mammal after disruption of corticospinal projections in the spinal cord.		
SQ SQ	Sequence 241 AA;		
Oy	Query Match 99.8%; Score 1265; DB 20; Length 241; Best Local Similarity 99.6%; Pred. No. 1.6e-133; Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Dd	1 MSMLFYLLIAPFLIGIOAEPHSESNVAGHTIPGVHWTKLQHSLDIPLRRARSPAAAIA 60 		
Oy	61 ARVAGOTRNVTPRLFKGRRLRSPEVLFSSTOPREAADODDFEVGGAAPERTHRSK 120 		
Dd	61 ARVAGGTNRITVPBRLEPKGRRLSPKLVETOPPREAADODDFEVGGAAPPRTTRSR 120 		
Oy	121 RSSSHPIFHGEFSSVCDSVSWWGDKTTATDINGKEVMVLGBVNINNSVFKEYFFETKR 180 		
Dd	121 RSSSSHPIFHGEFSSVCDSVSWWGDKTTATDINGKEVMVLGBVNINNSVFKEYFFETKR 180 		
Oy	181 DPPPVSGCGRGIDSKMNSYCTTHTFVALLTMGQAAAFRIIDPACVCVSRAVR 240 		

DB 181 DENPVDSCRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVLSKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9
 AAB66929
 ID AAB66929 standard; Protein; 241 AA.
 AC AAB66929;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Human NGF.
 XX
 XX Human; neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's chorea; nerve damage; nerve growth factor; NGF.
 OS Homo sapiens.
 XX
 PN US6174701-B1.
 XX
 PD 16-JAN-2001.
 XX
 PF 31-MAY-1995; 95US-0455741.
 XX
 PR 15-MAR-1990; 90US-0494024.
 PR 31-JAN-1995; 95US-0381030.
 PR 12-DEC-1989; 89US-0449811.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Rosenthal A, Winelow JW;
 XX
 DR MPI; 2001-201803/20.
 XX
 PT New nucleic acid encoding a neuronal factor (rat precursor
 PT neurotrophin-3, NT-3), useful in the recombinant preparation of NT-3,
 PT which is useful for enhancing the survival of nerve cells and treating
 PT neurodegenerative diseases
 XX
 PS Disclosure; Fig 3; 18bp; English.
 XX
 CC The present invention relates to neuronal factor (NF; also known as
 CC neurotrophin-3/NT-3; see AAF55829-AAF55830 and AAB66929-AA66928). NF
 CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's chorea, and other conditions
 CC characterized by necrosis or loss of neurons. NF is also useful for
 CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such
 CC as burns or wounds. The present sequence is human nerve growth factor
 CC (NGF), which was used in a sequence homology alignment with human NF
 CC protein.
 CC
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 22; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLLITAFILGIOAEHPHSESNVPAAGTTIPQVHWTXQHSIDTLARRARSPAAIA 60
 DB 1 MSMLFYLLITAFILGIOAEHPHSESNVPAAGTTIPQVHWTXQHSIDTLARRARSPAAIA 60
 QY 61 ARVAGGTNTITVDPRLFKKRLRSPRYLFTSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 DB 61 ARVAGGTNTITVDPRLFKKRLRSPRYLFTSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 QY 121 RSSHPHIFHKGESFVSDSVYVWGDKTATDICKKEVWVLGEVWVINSVFQYFFETKCR 180
 DB 121 RSSHPHIFHKGESFVSDSVYVWGDKTATDICKKEVWVLGEVWVINSVFQYFFETKCR 180

QY 181 DENPVDSCRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVLSKAVR 240
 DB 181 DENPVDSCRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVLSKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10
 AAE18904
 ID AAE18904 standard; Protein; 241 AA.
 AC AAE18904;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human beta nerve growth factor (NGF) protein.
 XX
 KW Human; nerve growth factor; NGF; neurotrophin; cholinergic neuron;
 KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;
 KW neurodegenerative condition; ALS; amyotrophic lateral sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200207774-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 17-MAY-2001; 2001WO-US16122.
 XX
 PR 19-JUL-2000; 2000US-0620174.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tuszynski MH;
 XX
 DR MPI; 2002-195846/25.
 DR N-PSDB; AAD30144.
 XX
 PT Delivering therapeutic neurotrophin to targeted defective, diseased or
 PT damaged cholinergic neurons, useful for treating neurodegenerative
 PT disease, comprises administering a neurotrophin encoding transgene into
 PT the brain
 XX
 PS Example 1; Fig 2; 38bp; English.
 XX
 CC The invention relates to a method for delivering therapeutic neurotrophin
 CC to targeted defective, diseased or damaged cholinergic neurons in
 CC the mammalian brain. The method comprises delivering a neurotrophin
 CC composition comprising a neurotrophin encoding transgene into one or more
 CC delivery sites within a region of the brain containing targeted neurons.
 CC The method is useful for treating neurodegenerative conditions such as
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis
 CC (ALS) in primates by stimulating the growth of neurons thus recovering
 CC neurological function. The present sequence is human nerve growth factor
 CC (NGF-2) protein which is a neurotrophin.
 CC
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 23; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLLITAFILGIOAEHPHSESNVPAAGTTIPQVHWTXQHSIDTLARRARSPAAIA 60
 DB 1 MSMLFYLLITAFILGIOAEHPHSESNVPAAGTTIPQVHWTXQHSIDTLARRARSPAAIA 60
 QY 61 ARVAGGTNTITVDPRLFKKRLRSPRYLFTSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 DB 61 ARVAGGTNTITVDPRLFKKRLRSPRYLFTSTQPREAADTODLDFEVGGAAPFRTTRSK 120

QY 121 RSSSHPIFRHGEFSCDSVSWVGDKTTATDICKENYVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSCDSVSWVGDKTTATDICKENYVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGCGIDSKHNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
 DB 181 DPNPVDSCGCGIDSKHNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 11
 ABB04994
 ID ABB04994 standard; Protein; 241 AA.
 XX ABB04994;
 AC
 DT 19-MAR-2002 (first entry)
 XX
 DE Human beta nerve growth factor protein.
 XX
 KM Human; nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;
 KM neurotrophin-3; nervous system growth factor; neuronal atrophy;
 KM aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;
 KM anti-aging; cholinergic neuron growth stimulator; gene therapy.
 OS Homo sapiens.
 XX
 PN US2001043920-A1.
 PD 22-NOV-2001.
 XX
 PF 05-DEC-2000; 2000US-0730790.
 XX
 PR 15-APR-1998; 98US-0060543.
 XX
 PA (TUSZ/) TUSZYNSKI M H.
 PA (BLES/) BLESCH A.
 PI Tuszynski MH, Blesch A;
 XX
 DR WPI; 2002-105567/14.
 DR N-PSDB; ABA92503.
 XX
 PT Ameliorating neuronal atrophy and loss of accompanying normal aging
 PT comprises delivering a transgene encoding a growth factor to a
 PT mammalian brain to stimulate axon growth in cholinergic neurons
 XX
 PS Disclosure; Fig 6 1-2; 18pp; English.
 XX
 CC The present invention describes a method for ameliorating neuronal
 CC atrophy and loss of accompanying normal aging in the mammalian brain.
 CC The method comprises delivering a growth factor (GF)-encoding transgene
 CC to preslected delivery sites in the brain, so that the encoded GF is
 CC expressed in the brain and stimulates axonal growth in targeted
 CC GF-receptive neurons. The growth factor has neurotrophic, neuroprotective
 CC and anti-aging activities, and can be used as a cholinergic neuron
 CC growth stimulator and in gene therapy. The method is used to
 CC ameliorating neuronal atrophy and loss of accompanying normal aging, in
 CC the human brain. The present sequence represents human beta nerve growth
 CC factor, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 23; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60
 DB 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60

QY 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60
 DB 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60

QY 61 ARVAGOTRNITVDBRLFEKRLRSPRVLFSTQPPREADTODLDFEVGGAAPRSRTHRSK 120
 DB 61 ARVAGOTRNITVDBRLFEKRLRSPRVLFSTQPPREADTODLDFEVGGAAPRSRTHRSK 120
 QY 121 RSSSHPIFRHGEFSCDSVSWVGDKTTATDICKENYVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSCDSVSWVGDKTTATDICKENYVLGEVNNINSVFKQYFFETKCR 180
 QY 241 A 241
 DB 241 A 241
 RESULT 12
 AAP40038
 ID AAP40038 standard; Protein; 245 AA.
 XX AAP40038;
 AC
 DT 25-JAN-1992 (first entry)
 XX
 DE Sequence encoded by portion of human beta-nerve growth factor
 DE (NGF) chromosomal gene which includes an exon.
 OS Homo sapiens.
 XX
 PN EP121338-A.
 PD 10-OCT-1984.
 XX
 PF 02-MAR-1984; 84EP-0301377.
 XX
 PR 03-MAR-1983; 83US-0471962.
 XX
 PA (GETH) GENENTECH INC.
 PI Gray AM, Ullrich A;
 XX
 DR WPI; 1984-251909/41.
 DR N-PSDB; AAN40033.
 XX
 PT Human beta-nerve growth factor free from other proteins - obtd.
 PT by recombinant DNA techniques for treating nerve damage
 XX
 PS Example; Fig 5; 42pp; English.
 XX
 CC The inventors claim human beta-nerve growth factor (NGF) free from
 CC other proteins of human origin. Also claimed are the DNA sequence
 CC encoding human beta-NGF operably linked with a DNA sequence capable
 CC of effecting its expression in a recombinant host cell; a replicable
 CC expression vector contg. the DNA; and host cells transformed with
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
 CC the plasmid, larger amounts of pure beta-NGF are obtainable than by
 CC extrn. of natural materials, see e.g. EP--2139.
 XX
 SQ Sequence 245 AA;
 Query Match 99.8%; Score 1265; DB 5; Length 245;
 Best Local Similarity 99.6%; Pred. No. 1.7e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60
 DB 5 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 64
 QY 61 ARVAGOTRNITVDBRLFEKRLRSPRVLFSTQPPREADTODLDFEVGGAAPRSRTHRSK 120

QY 1 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 60
 DB 5 MSMTLFTTLTATLIGIOAEPHSESNNVPAGHTTIPQVHWTKLQHSIDTALRRARSAPAAIA 64

Db 65 ARVAGQTRNITVDPLFKKRLRSPVLFSTQPPREAADTODLDEVEVGAAPFNTRHSK 124
 Qy 121 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 180
 Db 125 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 184
 Qy 181 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 240
 Db 185 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 244
 Qy 241 A 241
 Db 245 A 245

RESULT 13

AAR45241
 ID AAR45241 standard; Protein; 307 AA.

AC AAR45241;
 DT 20-JUN-1994 (first entry)
 DE Human pre-pro nerve growth factor.
 KW Mature; beta-nerve growth factor; pre-pro portion; expression; NGF; hNGF; treatment; Alzheimer's Disease.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT Peptide 1..187.
 FT Peptide /note= "signal peptide"
 FT Peptide 188..307
 FT Peptide /note= "mature peptide"
 PN US5272063-A.
 PD 21-DEC-1993.
 PF 20-JUN-1989; 89US-0383118.
 PR 22-NOV-1988; 88US-0274878.
 PR 20-JUL-1989; 89US-0383118.
 PA (SYNT) SYNTAX USA INC.
 PI Baecker PA, Barnett JW, BursztyN-Pettegrew H, Chan HW, Nguyen BT, Ward C;
 DR WPI; 1993-413401/51.
 DR N-PSDB; AAO54283.
 PT Prodn. of active mature human beta-nerve growth factor in insect cells; using baculovirus expression system, and potential use of recombinant hNGF in treatment of Alzheimer's disease
 PS Disclosure; Fig 1; 23pp; English.
 CC The sequence is that of human pre-pro nerve growth factor which was used in a method of producing biologically active mature human beta-nerve growth factor in insect cells.
 SQ Sequence 307 AA;

Query Match 99.5%; Score 1262; DB 1; Length 307;
 Best Local Similarity 99.2%; Pred. No. 5e-133;
 Matches 239; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMEFYTLITAFILGICQEPHSESNVPAGHTIPQVHWTKLOHSLDTLRARSAAPAAIA 60
 Db 67 MSMEFYTLITAFILGICQEPHSESNVPAGHTIPQVHWTKLOHSLDTLRARSAAPAAIA 126

Qy 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTQPPREAADTODLDEVEVGAAPFNTRHSK 120
 Db 127 ARVAGQTRNITVDPLFKKRLRSPVLFSTQPPREAADTODLDEVEVGAAPFNTRHSK 186
 Qy 121 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 180
 Db 187 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 246
 Qy 181 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 240
 Db 247 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 306
 Qy 241 A 241
 Db 307 A 307

RESULT 14

AAB67865
 ID AAB67865 standard; Protein; 241 AA.

AC AAB67865;
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human polypeptide designated PTMA-8.

KW PTMA; immune deficiency; infection; autoimmune disorder; wound closure; connective tissue disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host disease; autoimmune inflammatory eye disease; gut protection; gut regeneration; fibrosis; reperfusion injury; systemic cytokine damage.

OS Homo sapiens.
 PN WO200123572-A2.
 PD 05-APR-2001.
 PF 29-SEP-2000; 2000WO-US41035.
 PR 30-SEP-1999; 99US-0156745.
 PR 06-OCT-1999; 99US-0158942.
 PR 13-OCT-1999; 99US-0159248.
 PR 06-DEC-1999; 99US-0169344.
 PR 29-JUN-2000; 2000US-0215048.
 PA (CURA-) CURAGEN CORP.
 PI Prayaga SK, Vernet C, Shinkete RA, Burgess C, Spytek KA;
 DR WPI; 2001-273512/28.
 DR N-PSDB; AAF60462.

PT Novel polypeptides termed PTMAX, and nucleic acids encoding PTMAX, useful for detecting and treating diseases caused immune deficiencies -
 PS Claim 1; Page 20-22; 128pp; English.

CC The present sequence represents a PTMA-8 (not defined) polypeptide. The sequence is derived from clone AL049825. The polypeptide is 2658.5 daltons. PTMA polynucleotides and polypeptides are used in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated with PTMA. They may be useful in the treatment of various immune deficiencies and disorders. These immune deficiencies may be genetic or caused by viral as well as bacterial or fungal infections or may result from autoimmune disorders. Autoimmune disorders which may be treated using PTMA include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
 CC and autoimmune inflammatory eye disease. Additionally PTMA may also be
 CC useful to promote better or faster closure of non-healing wounds,
 CC including pressure ulcers, ulcers associated with vascular insufficiency,
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissue, and conditions resulting from
 CC systemic cytokine damage.

XX Sequence 241 AA;

Query Match 99.4%; Score 1261; DB 22; Length 241;
 Best Local Similarity 99.2%; Pred. No. 4,6e-133;

Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLPYTLITAFLLIGIOAEPHSESNVPAGHTIPVHWTKLOHSIDLTLARRASAPAAIA 60
 DB 1 MSMLPYTLITAFLLIGIOAEPHSESNVPAGHTIPVHWTKLOHSIDLTLARRASAPAAIA 60
 QY 61 ARVAGQNTITVDRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFSTTRSK 120
 DB 61 ARVAGQNTITVDRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFSTTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFETKCR 180
 QY 181 DPNVDGCGRIGIDSKHNSYCTTHTFFVKALTMDSQAAPFIRIDTACVLSKAVR 240
 DB 181 DPNVDGCGRIGIDSKHNSYCTTHTFFVKALTMDSQAAPFIRIDTACVLSKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 15

AAR37799 standard; Protein; 307 AA.

XX AAR37799;
 AC
 XX 23-SEP-1993 (first entry)
 DT
 XX
 DE Human NGF.

XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;
 KW BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;
 KW central; precursor; nervous system.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..187
 FT /note="Prepro region"
 FT Protein 188..307
 FT /note="Mature NGF"

XX MO9310150-A.

XX 27-MAY-1993.

XX 13-NOV-1992; 92MO-US09792.

XX 14-NOV-1991; 91US-0792492.

XX (AMGS-) AMGEN.
 PA (REG-) REGENERON PHARM INC.

PI Gies D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;
 XX WPI; 1993-182492/22.

DR N-PSDB; AAQ42571.

XX
 XX
 PT Eukaryotic expression of neurotrophins - using prepro region of a
 PT different neurotrophin for more efficient post-translational
 PT processing

XX Disclosure; Fig 4; 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein
 CC encoded by this sequence promotes the development of the peripheral
 CC nervous system and also influences the development and maintenance of
 CC specific populations of neurons in the central nervous system. Two
 CC major transcripts from the NGF gene result in a "long" and "short" NGF
 CC prepropeptide. The "short" precursor contains a conventional signal
 CC sequence at the N-terminus which flanks the pro-region. The "long"
 CC precursor contains an additional "pro-region" at its N-terminal. No
 CC functional distinction has been elucidated between the "long" and
 CC "short" forms. Characteristics of NGF, such as isoelectric point and
 CC primary structure, are very similar to brain derived neurotrophic
 CC factor (BDNF). The NGF coding sequence may be used in the
 CC construction of a chimeric nucleic acid molecule to encode a prepro-
 CC NGF/BDNF chimera (see also AAQ42568-69).

XX Sequence 307 AA;

Query Match 99.4%; Score 1261; DB 14; Length 307;
 Best Local Similarity 99.2%; Pred. No. 6,5e-133;

Matches 239; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLPYTLITAFLLIGIOAEPHSESNVPAGHTIPVHWTKLOHSIDLTLARRASAPAAIA 60
 DB 67 MSMLPYTLITAFLLIGIOAEPHSESNVPAGHTIPVHWTKLOHSIDLTLARRASAPAAIA 126
 QY 61 ARVAGQNTITVDRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFSTTRSK 120
 DB 127 ARVAGQNTITVDRLFKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFSTTRSK 186
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFETKCR 180
 DB 187 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFETKCR 246
 QY 181 DPNVDGCGRIGIDSKHNSYCTTHTFFVKALTMDSQAAPFIRIDTACVLSKAVR 240
 DB 247 DPNVDGCGRIGIDSKHNSYCTTHTFFVKALTMDSQAAPFIRIDTACVLSKAVR 306
 QY 241 A 241
 DB 307 A 307

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